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OM protein - protein search, using sw model

Run on: August 22, 2005, 14:31:14 ; Search time 171 Seconds

(without alignments)
29.403 Million cell updates/sec

Title: US-10-639-076-4
Perfect score: 89
Sequence: 1 MEVLCTWETCER 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: A_Geneseq_16Dec04:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	89	100.0	13 4	AAB90146 Factor VI
2	89	100.0	13 6	ABR82342 Factor X
3	89	100.0	13 8	ABR82342 Tissue fa
4	89	100.0	15 4	ABR82341 Factor X
5	89	100.0	15 6	ABR82341 Tissue fa
6	89	100.0	15 8	ADM96581 Tissue fa
7	89	100.0	15 8	ADM96581 Tissue fa
8	89	100.0	15 8	ADM96582 Tissue fa
9	89	100.0	15 8	ADM96594 Tissue fa
10	89	100.0	16 4	ABR82340 Factor X
11	89	100.0	16 6	ABR82340 Tissue fa
12	89	100.0	18 4	AAB90160 Factor VI
13	89	100.0	18 6	ABR82338 Factor X
14	89	100.0	18 6	ABR82338 Tissue fa
15	89	100.0	20 6	ABR82337 Factor X
16	89	100.0	22 4	AAB90199 Factor VI
17	89	100.0	22 4	AAB90182 Factor VI
18	89	100.0	24 4	AAB90181 Factor VI
19	89	100.0	24 4	AAB90183 Factor VI
20	89	100.0	24 4	AAB90169 Factor VI
21	89	100.0	24 4	AAB90168 Factor VI
22	89	100.0	24 4	AAB90161 Factor VI
23	89	98.9	15 8	ADM96595 Tissue fa
24	88	98.9	24 4	AAB90184 Factor VI
25	87	97.8	15 8	ADM96596 Tissue fa

26	87	97.8	15 8	ADM96597 Tissue fa
27	87	97.8	24 4	AAB90185 Factor VI
28	87	97.8	24 4	AAB90186 Factor VI
29	86	96.6	13 4	AAB90147 Factor VI
30	86	96.6	15 8	ADM96605 Tissue fa
31	86	96.6	15 8	ADM96598 Tissue fa
32	86	96.6	15 8	ADM96606 Tissue fa
33	86	96.6	24 4	AAB90194 Factor VI
34	86	96.6	24 4	AAB90187 Factor VI
35	86	96.6	24 4	AAB90195 Factor VI
36	85	95.5	15 8	ADM96585 Tissue fa
37	85	95.5	15 8	ADM96591 Tissue fa
38	84	94.4	12 6	ABR82347 Factor X
39	84	94.4	15 8	ADM96604 Tissue fa
40	84	94.4	15 8	ADM96607 Tissue fa
41	84	94.4	15 8	ADM96608 Tissue fa
42	84	94.4	15 8	ADM96593 Tissue fa
43	84	94.4	15 8	ADM96591 Tissue fa
44	84	94.4	15 8	ADM96586 Tissue fa
45	84	94.4	15 8	ADM96588 Tissue fa
46	84	94.4	24 4	AAB90196 Factor VI
47	84	94.4	24 4	AAB90175 Factor VI
48	84	94.4	24 4	AAB90197 Factor VI
49	84	94.4	24 4	AAB90180 Factor VI
50	84	94.4	24 4	AAB90193 Factor VI
51	84	94.4	24 4	AAB90207 Factor VI
52	84	94.4	24 4	AAB90173 Factor VI
53	84	94.4	24 4	AAB90178 Factor VI
54	83	93.3	13 4	AAB90145 Factor VI
55	83	93.3	15 8	ADM96590 Tissue fa
56	83	93.3	15 8	ADM96584 Tissue fa
57	83	93.3	15 8	ADM96592 Tissue fa
58	83	93.3	24 4	AAB90171 Factor VI
59	83	93.3	24 4	AAB90177 Factor VI
60	83	93.3	24 4	AAB90179 Factor VI
61	82	92.1	18 4	AAB90219 Factor VI
62	82	92.1	20 4	AAB90237 Factor VI
63	82	92.1	20 4	AAB90231 Factor VI
64	81	91.0	18 4	AAB90220 Factor VI
65	80	89.9	15 8	ADM96615 Tissue fa
66	80	89.9	15 8	ADM96617 Tissue fa
67	80	89.9	15 8	ADM96616 Tissue fa
68	80	89.9	24 4	AAB90204 Factor VI
69	80	89.9	24 4	AAB90205 Factor VI
70	80	89.9	24 4	AAB90206 Factor VI
71	79	88.8	11 6	ABR82348 Factor X
72	79	88.8	15 8	ADM96611 Tissue fa
73	79	88.8	15 8	ADM96599 Tissue fa
74	79	88.8	15 8	ADM96602 Tissue fa
75	79	88.8	15 8	ADM96613 Tissue fa
76	79	88.8	22 4	AAB90202 Factor VI
77	79	88.8	24 4	AAB90200 Factor VI
78	79	88.8	24 4	AAB90191 Factor VI
79	79	88.8	24 4	AAB90188 Factor VI
80	78	87.6	12 6	ABR82343 Factor X
81	78	87.6	15 8	ADM96583 Tissue fa
82	78	87.6	15 8	ADM96612 Tissue fa
83	78	87.6	18 4	AAB90218 Factor VI
84	78	87.6	18 4	AAB90221 Factor VI
85	78	87.6	20 4	AAB90209 Factor VI
86	78	87.6	20 4	AAB90215 Factor VI
87	78	87.6	20 6	ABR82332 Factor X
88	78	87.6	20 6	ABR82331 Factor X
89	78	87.6	24 4	AAB90170 Factor VI
90	78	87.6	24 4	AAB90201 Factor VI
91	77	86.5	13 4	AAB90224 Factor VI
92	77	86.5	15 8	ADM96601 Tissue fa
93	77	86.5	24 4	AAB90190 Factor VI
94	76	85.4	13 4	AAB90229 Factor VI
95	76	85.4	15 8	ADM96603 Tissue fa
96	76	85.4	15 8	ADM96600 Tissue fa
97	76	85.4	18 4	AAB90222 Factor VI
98	76	85.4	20 4	AAB90214 Factor VI

99 76 85.4 20 6 ABR82329 ABr82329 Clone AE
100 76 85.4 24 4 AAB90192 AAB90192 Factor VI

ALIGNMENTS

RESULT 1
AAB90146
ID AAB90146 standard; peptide; 13 AA.

AC AAB90146;

DT 23-MAY-2001 (first entry)

DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 4.

XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX chronic thrombembolic disease; fibrin formation; vascular disorder;
XX deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX septicemia; hypotension; angioedema; ARDS.

OS Synthetic.

PN WO200110892-A2.

PD 15-FEB-2001.

PF 04-AUG-2000; 2000WO-US021296.

PR 06-AUG-1999; 99US-0147627P.

PR 23-AUG-1999; 99US-0150315P.

PA (GENTH) GENENTECH INC.

PI Dennis MS;

DR WPI; 2001-211069/21.

PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods; inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.

PS Claim 1; Page 49; 80pp; English.

XX This invention relates to peptides which act as antagonist of Factor VIIa
XX (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX activity in the presence of a tissue factor (TF) and for treating a
XX TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX treated include chronic thrombembolic diseases or disorders associated
XX with fibrin formation including vascular disorders such as deep venous
XX thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX arteriosclerosis and restenosis following angioplasty, acute and chronic
XX indications such as inflammation, septic shock, septicemia, hypotension,
XX cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX distress syndrome (ARDS), disseminated intravascular coagulation (DIC)
XX and other diseases like inflammatory disorders. The antagonist peptides
XX are also useful in research, and for diagnostic, therapeutic and
XX prophylactic purposes. The present sequence represents a factor VIIa
XX antagonist peptide of the invention

SQ Sequence 13 AA;

Query Match 100.0%; Score 89; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVLQWTWETCER 13

DB 1 MEVLQWTWETCER 13

RESULT 2
ABR82342
ID ABR82342 standard; peptide; 13 AA.

AC ABR82342;

DT 06-NOV-2003 (first entry)

DE Factor X activation inhibiting A-series peptide A-65.

XX Soyasacatin N; scN; cybetatin; negative cross resistance toxin; NCR;
XX factor X.

OS Synthetic.

PN WO2003060463-A2.

PD 24-JUL-2003.

PF 30-JUL-2002; 2002WO-US024216.

PR 30-JUL-2001; 2001US-0308790P.

PR 20-AUG-2001; 2001US-0313608P.

PR 21-AUG-2001; 2001US-0313854P.

PR 14-SEP-2001; 2001US-032227P.

PA (PURD) PURDUE RES FOUND.

PA (PITT/) PITTDNRIGH B R.

PA (MURD/) MURDOCK L L.

PA (GAF/) GAFNEY P J.

PI Pittendriigh BR, Murdock LL, Gaffney PJ;

DR WPI; 2003-598567/56.

PT Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.

PS Example; Fig 24; 124pp; English.

XX The invention relates to evaluating the efficacy of molecule against a
XX target population including a pest strain resistant to first toxin. The
XX method involves determining pest strain susceptible to the first toxin,
XX selecting strain resistant to first toxin, and evaluating the efficacy of
XX resistant strain with molecules to determine second toxin that is more
XX toxic to resistant strain than to susceptible strain. The resistant and
XX susceptible strains co-exist in the target population. The method is
XX useful for evaluating the efficacy of molecule against a target
XX population comprising pest strain resistant to first toxin, e.g. insect
XX population, mammalian population, plant population, animal population, or
XX virus population. The efficacy of molecules to kill unwanted resistant
XX organisms is increased. Sequences ABR82336-49 represent A-series peptides
XX that inhibit the activation of factor X

SQ Sequence 13 AA;

Query Match 100.0%; Score 89; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVLQWTWETCER 13

DB 1 MEVLQWTWETCER 13

RESULT 3

ADM96618
ID ADM96618 standard; peptide; 13 AA.

AC ADM96618;

XX 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #40.
 XX
 KM tissue factor VIIa; tFVIIa; chronic thromboembolic disease;
 KM fibrin formation; vascular disorders; deep venous thrombosis;
 KM arterial thrombosis; stroke; atherosclerosis; septicemia.
 XX
 OS Synthetic.
 XX
 PN US2004087767-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 PR 06-FEB-2002; 2002US-0355420P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lazarus RA, Maun HR;
 XX
 DR WPI; 2004-356247/33.
 XX
 PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 PS Disclosure; SEQ ID NO 40; 102pp; English.
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 13 AA;
 XX
 QY
 Db 1 MEVLQWTWETCER 13
 1 MEVLQWTWETCER 13
 Query Match 100.0%; Score 89; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PD 15-FEB-2001.
 XX
 PF 04-AUG-2000; 2000MO-US021296.
 XX
 PR 06-AUG-1999; 99US-0147627P.
 PR 23-AUG-1999; 99US-0150315P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dennis MS;
 XX
 DR WPI; 2001-211069/21.
 XX
 PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX
 PS Example 1; Fig 4; 80pp; English.
 XX
 CC This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TE/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thromboembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumor metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 SQ Sequence 15 AA;
 XX
 QY
 Db 1 MEVLQWTWETCER 13
 3 MEVLQWTWETCER 15
 Query Match 100.0%; Score 89; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 AAB90165
 ID AAB90165 standard; peptide; 15 AA.
 XX
 AC AAB90165;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 23.
 XX
 KM Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KM chronic thromboembolic disease; fibrin formation; vascular disorder;
 KM deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KM thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KM septicemia; hypotension; angioedema; ARDS.
 XX
 OS Synthetic.
 XX
 PN WO200110892-A2.
 XX

RESULT 5
 ABR82341
 ID ABR82341 standard; peptide; 15 AA.
 XX
 AC ABR82341;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Factor X activation inhibiting A-series peptide A-183.
 XX
 KM Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
 KM factor X.
 XX
 OS Synthetic.
 XX
 PN WO2003060463-A2.
 XX
 PD 24-JUL-2003.
 XX
 PF 30-JUL-2002; 2002MO-US024216.
 XX
 PR 30-JUL-2001; 2001US-0308790P.
 PR 20-AUG-2001; 2001US-0313608P.
 PR 21-AUG-2001; 2001US-0313654P.
 PR 14-SEP-2001; 2001US-0322227P.
 XX

PA (PURD) PURDUE RES FOUND.
 PA (PITT/) PITTEMDRIGH B R.
 PA (MURD/) MURDOCK L L.
 PA (GAF/) GAFNEY P J.
 PI Pittemdrigh BR, Murdock LL, Gaffney PJ;
 DR WPI; 2003-598567/56.
 XX
 XX
 PT Evaluating the efficacy of molecule against target population including
 PT toxin-resistant pest strain, by determining susceptible pest strain,
 PT selecting resistant strain, and evaluating efficacy of resistant strain
 PT with molecules.
 PS
 XX Example; Fig 24; 124pp; English.
 CC The invention relates to evaluating the efficacy of molecule against a
 CC target population including a pest strain resistant to first toxin. The
 CC method involves determining pest strain susceptible to the first toxin,
 CC selecting strain resistant to first toxin, and evaluating the efficacy of
 CC resistant strain with molecules to determine second toxin that is more
 CC toxic to resistant strain than to susceptible strain. The resistant and
 CC susceptible strains co-exist in the target population. The method is
 CC useful for evaluating the efficacy of molecule against a target
 CC population comprising pest strain resistant to first toxin, e.g. insect
 CC population, mammalian population, plant population, animal population, or
 CC virus population. The efficacy of molecules to kill unwanted resistant
 CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
 CC that inhibit the activation of factor X
 CC
 CC
 CC Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 89; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WEVLCTWETCER 13
 |||||
 |||||
 Db 3 WEVLCTWETCER 15
 |||||
 |||||
 RESULT 6
 ADM96610
 ID ADM96610 standard; peptide; 15 AA.
 XX
 AC ADM96610;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #32.
 XX
 KM tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KM fibrin formation; vascular disorders; deep venous thrombosis;
 KM arterial thrombosis; stroke; atherosclerosis; septicaemia.
 XX
 OS Synthetic.
 XX
 PN US2004087767-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 PR 06-FEB-2002; 2002US-0355420P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lazarus RA, Maun HR;
 XX
 DR WPI; 2004-356247/33.
 XX
 PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular

PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 XX Disclosure; SEQ ID NO 32; 102pp; English.
 PS
 XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 CC
 CC
 CC Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 WEVLCTWETCER 13
 |||||
 |||||
 Db 1 WEVLCTWETCER 13
 |||||
 |||||
 RESULT 7
 ADM96581
 ID ADM96581 standard; peptide; 15 AA.
 XX
 AC ADM96581;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #3.
 XX
 KM tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KM fibrin formation; vascular disorders; deep venous thrombosis;
 KM arterial thrombosis; stroke; atherosclerosis; septicaemia.
 XX
 OS Synthetic.
 XX
 PN US2004087767-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 PR 06-FEB-2002; 2002US-0355420P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lazarus RA, Maun HR;
 XX
 DR WPI; 2004-356247/33.
 XX
 PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 PS Disclosure; SEQ ID NO 3; 102pp; English.
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
 |||||
 Db 3 WEVLCTWETCER 15

RESULT 8

ADM96582 standard; peptide; 15 AA.

AC ADM96582;

DT 29-JUL-2004 (first entry)

DE Tissue factor VIIa (tFVIIa) peptide antagonist #4.

KW tissue factor VIIa; tFVIIa; chronic thromboembolic disease;
 KM fibrin formation; vascular disorders; deep venous thrombosis;
 XX arterial thrombosis; stroke; atherosclerosis; septicemia.

OS Synthetic.

PN US2004087767-A1.

PD 06-MAY-2004.

PS 30-JAN-2003; 2003US-00356257.

PR 06-FEB-2002; 2002US-0355420P.

PA (GETH) GENENTECH INC.

PI Lazarus RA, Maun HR;

DR WPI; 2004-356247/33.

PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

PS Disclosure; SEQ ID NO 4; 102pp; English.

CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
 |||||
 Db 3 WEVLCTWETCER 15

RESULT 9

ADM96594 standard; peptide; 15 AA.

AC ADM96594;

AC ADM96594;
 DT 29-JUL-2004 (first entry)

DE Tissue factor VIIa (tFVIIa) peptide antagonist #16.

KW tissue factor VIIa; tFVIIa; chronic thromboembolic disease;
 KM fibrin formation; vascular disorders; deep venous thrombosis;
 XX arterial thrombosis; stroke; atherosclerosis; septicemia.

OS Synthetic.

PN US2004087767-A1.

PD 06-MAY-2004.

PS 30-JAN-2003; 2003US-00356257.

PR 06-FEB-2002; 2002US-0355420P.

PA (GETH) GENENTECH INC.

PI Lazarus RA, Maun HR;

DR WPI; 2004-356247/33.

PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

PS Claim 1; SEQ ID NO 16; 102pp; English.

CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
 |||||
 Db 3 WEVLCTWETCER 15

RESULT 10

AAB90159 standard; peptide; 16 AA.

AC AAB90159;

DT 23-MAY-2001 (first entry)

DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 17.

KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KM chronic thromboembolic disease; fibrin formation; vascular disorder;
 KM deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KM thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KM septicemia; hypotension; angioedema; ARDS.

OS Synthetic.

PN WO200110892-A2.

XX 15-FEB-2001.
PD ABR82340
XX ABR82340 standard; peptide; 16 AA.
XX
PF 04-AUG-2000; 2000MO-US021296.
XX
PR 06-AUG-1999; 99US-0147627P.
XX 23-AUG-1999; 99US-0150315P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dennis MS;
XX WPI; 2001-211069/21.
XX
DR WPI; 2001-211069/21.
XX
PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.
XX
PS Example 1; Fig 4; 80pp; English.
XX
CC This invention relates to peptides which act as antagonist of Factor VIIa
CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
CC activity in the presence of a tissue factor (TF) and for treating a
CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
CC treated include chronic thromboembolic diseases or disorders associated
CC with fibrin formation including vascular disorders such as deep venous
CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
CC arteriosclerosis and restenosis following angioplasty, acute and chronic
CC indications such as inflammation, septic shock, septicemia, hypotension,
CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
CC and other diseases like inflammatory disorders. The antagonist peptides
CC are also useful in research, and for diagnostic, therapeutic and
CC prophylactic purposes. The present sequence represents a factor VIIa
CC antagonist peptide of the invention
XX
SQ Sequence 16 AA;
XX
Query Match 100.0%; Score 89; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEVLCTWETCER 13
Db 2 WEVLCTWETCER 14
XX
RESULT 11
ABR82340
ID ABR82340 standard; peptide; 16 AA.
XX
AC ABR82340;
XX
DT 06-NOV-2003 (first entry)
XX
DE Factor X activation inhibiting A-series peptide A-99.
XX
KW Soyasactin N; scN; cystatin; negative cross resistance toxin; NCR;
KW factor X.
XX
OS Synthetic.
XX
PN WO2003060463-A2.
XX
PD 24-JUL-2003.
XX
PF 30-JUL-2002; 2002MO-US024216.
XX
PR 30-JUL-2001; 2001US-0308790P.
XX 20-AUG-2001; 2001US-0313608P.
XX 21-AUG-2001; 2001US-0313854P.
XX 14-SEP-2001; 2001US-0322227P.
XX

XX (PURD) PURDUE RES FOUND.
PA (PITT/) PITTEMDRIGH B R.
PA (MURD/) MURDOCK L L.
PA (GAFF/) GAFFNEY P J.
XX
PI Pittendrigh BR, Murdock LL, Gaffney PJ;
XX WPI; 2003-598567/56.
XX
XX
XX Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.
XX
PS Example; Fig 24; 124pp; English.
XX
XX The invention relates to evaluating the efficacy of molecule against a
CC target population including a pest strain resistant to first toxin. The
CC method involves determining pest strain susceptible to the first toxin,
CC selecting strain resistant to first toxin, and evaluating the efficacy of
CC resistant strain with molecules to determine second toxin that is more
CC toxic to resistant strain than to susceptible strain. The resistant and
CC susceptible strains co-exist in the target population. The method is
CC useful for evaluating the efficacy of molecule against a target
CC population comprising pest strain resistant to first toxin, e.g. insect
CC virus population. The efficacy of molecules to kill unwanted resistant
CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
CC that inhibit the activation of factor X
XX
SQ Sequence 16 AA;
XX
Query Match 100.0%; Score 89; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEVLCTWETCER 13
Db 2 WEVLCTWETCER 14
XX
RESULT 12
AAB90160
ID AAB90160 standard; peptide; 18 AA.
XX
AC AAB90160;
XX
DT 23-MAY-2001 (first entry)
XX
DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 18.
XX
KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thromboembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
KW septicemia; hypotension; angioedema; ARDS.
XX
OS Synthetic.
XX
PN WO200110892-A2.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000MO-US021296.
XX
PR 06-AUG-1999; 99US-0147627P.
XX 23-AUG-1999; 99US-0150315P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dennis MS;
XX



DR WPI; 2001-211069/21.
XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.
XX
PS Example 1; Fig 4; 80pp; English.
XX
CC This invention relates to peptides which act as antagonist of Factor VIIa
CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
CC activity in the presence of a tissue factor (TF) and for treating a
CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
CC treated include chronic thromboembolic diseases or disorders associated
CC with fibrin formation including vascular disorders such as deep venous
CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
CC arteriosclerosis and restenosis following angioplasty, acute and chronic
CC indications such as inflammation, septic shock, septicemia, hypotension,
CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
CC and other diseases like inflammatory disorders. The antagonist peptides
CC are also useful in research, and for diagnostic, therapeutic and
CC prophylactic purposes. The present sequence represents a Factor VIIa
CC antagonist peptide of the invention
XX
SQ Sequence 18 AA;
OY
Query Match 100.0%; Score 89; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MEVLCTWETCER 13
3 MEVLCTWETCER 15
RESULT 13
ABR82338
ID ABR82338 standard; peptide; 18 AA.
XX
AC ABR82338;
XX
DT 06-NOV-2003 (first entry)
XX
DE Factor X activation inhibiting A-series peptide A-100-Z.
XX
KM Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
XX factor X.
XX
OS Synthetic.
XX
FN WO2003060463-A2.
XX
PD 24-JUL-2003.
XX
PF 30-JUL-2002; 2002WO-US024216.
XX
PR 30-JUL-2001; 2001US-0308790P.
XX 20-AUG-2001; 2001US-0313608P.
XX 21-AUG-2001; 2001US-0313854P.
XX 14-SEP-2001; 2001US-0322227P.
XX
PA (PURD) PURDUE RES. FOUND.
PA (PITT/) PITTDENDRIGH B R.
PA (MURD/) MURDOCK L L.
PA (GAFF/) GAFFNEY P J.
PI Pittendrigh BR, Murdock LL, Gaffney PJ;
XX WPI; 2003-598567/56.
XX
XX Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT

PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.
XX
PS Example; Fig 24; 124pp; English.
XX
CC The invention relates to evaluating the efficacy of molecule against a
CC target population including a pest strain resistant to first toxin. The
CC method involves determining pest strain susceptible to the first toxin,
CC selecting strain resistant to first toxin, and evaluating the efficacy of
CC resistant strain with molecules to determine second toxin that is more
CC toxic to resistant strain than to susceptible strain. The resistant and
CC susceptible strains co-exist in the target population. The method is
CC useful for evaluating the efficacy of molecule against a target
CC population comprising pest strain resistant to first toxin, e.g. insect
CC population, mammalian population, plant population, animal population, or
CC virus population. The efficacy of molecules to kill unwanted resistant
CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
CC that inhibit the activation of factor X
XX
SQ Sequence 18 AA;
OY
Query Match 100.0%; Score 89; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MEVLCTWETCER 13
3 MEVLCTWETCER 15
RESULT 14
ABR82339
ID ABR82339 standard; peptide; 18 AA.
XX
AC ABR82339;
XX
DT 06-NOV-2003 (first entry)
XX
DE Factor X activation inhibiting A-series peptide A-100.
XX
KM Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
XX factor X.
XX
OS Synthetic.
XX
FN WO2003060463-A2.
XX
PD 24-JUL-2003.
XX
PF 30-JUL-2002; 2002WO-US024216.
XX
PR 30-JUL-2001; 2001US-0308790P.
XX 20-AUG-2001; 2001US-0313608P.
XX 21-AUG-2001; 2001US-0313854P.
XX 14-SEP-2001; 2001US-0322227P.
XX
PA (PURD) PURDUE RES. FOUND.
PA (PITT/) PITTDENDRIGH B R.
PA (MURD/) MURDOCK L L.
PA (GAFF/) GAFFNEY P J.
PI Pittendrigh BR, Murdock LL, Gaffney PJ;
XX WPI; 2003-598567/56.
XX
XX Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.
XX
PS Example; Fig 24; 124pp; English.
XX
XX The invention relates to evaluating the efficacy of molecule against a

XX SQ Sequence 22 AA;
Query Match 100.0%; Score 89; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MEVLCTWTCR 13
1 MEVLCTWTCR 13
1 MEVLCTWTCR 13
RESULT 17
AAB90182
ID AAB90182 standard; peptide; 24 AA.
XX AAB90182;
AC AAB90182;
XX 23-MAY-2001 (first entry)
XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 40.
XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX chronic thrombolytic disease; fibrin formation; vascular disorder;
XX deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX septicemia; hypotension; angioedema; ARDS.
XX Synthetic.
XX WO200110892-A2.
XX 15-FEB-2001.
XX 04-AUG-2000; 2000MO-US021296.
XX 06-AUG-1999; 99US-0147627P.
XX 23-AUG-1999; 99US-0150315P.
XX (GETH) GENENTECH INC.
XX Dennis MS;
XX WPI; 2001-211069/21.
XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
XX and prophylactic methods, inhibits FVII/FVIIa mediated processes and
XX blocks initial events of blood coagulation.
XX Example 1; Fig 4; 80pp; English.
XX This invention relates to peptides which act as antagonist of Factor VIIa
XX (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX activity in the presence of a tissue factor (TF) and for treating a
XX TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX treated include chronic thrombolytic diseases or disorders associated
XX with fibrin formation including vascular disorders such as deep venous
XX thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX arteriosclerosis and restenosis following angioplasty, acute and chronic
XX indications such as inflammation, septic shock, septicemia, hypotension,
XX cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
XX and other diseases like inflammatory disorders. The antagonist peptides
XX are also useful in research, and for diagnostic, therapeutic and
XX prophylactic purposes. The present sequence represents a factor VIIa
XX antagonist peptide of the invention
XX Sequence 24 AA;
Query Match 100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVLCTWTCR 13
1 MEVLCTWTCR 13
1 MEVLCTWTCR 13
Db 3 MEVLCTWTCR 15
RESULT 18
AAB90181
ID AAB90181 standard; peptide; 24 AA.
XX AAB90181;
AC AAB90181;
XX 23-MAY-2001 (first entry)
XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 39.
XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX chronic thrombolytic disease; fibrin formation; vascular disorder;
XX deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX septicemia; hypotension; angioedema; ARDS.
XX Synthetic.
XX WO200110892-A2.
XX 15-FEB-2001.
XX 04-AUG-2000; 2000MO-US021296.
XX 06-AUG-1999; 99US-0147627P.
XX 23-AUG-1999; 99US-0150315P.
XX (GETH) GENENTECH INC.
XX Dennis MS;
XX WPI; 2001-211069/21.
XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
XX and prophylactic methods, inhibits FVII/FVIIa mediated processes and
XX blocks initial events of blood coagulation.
XX Example 1; Fig 4; 80pp; English.
XX This invention relates to peptides which act as antagonist of Factor VIIa
XX (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX activity in the presence of a tissue factor (TF) and for treating a
XX TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX treated include chronic thrombolytic diseases or disorders associated
XX with fibrin formation including vascular disorders such as deep venous
XX thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX arteriosclerosis and restenosis following angioplasty, acute and chronic
XX indications such as inflammation, septic shock, septicemia, hypotension,
XX cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
XX and other diseases like inflammatory disorders. The antagonist peptides
XX are also useful in research, and for diagnostic, therapeutic and
XX prophylactic purposes. The present sequence represents a factor VIIa
XX antagonist peptide of the invention
XX Sequence 24 AA;
Query Match 100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 19
ID AAB90183 standard; peptide; 24 AA.
XX
AC
XX AAB90183;
XX
DT 23-MAY-2001 (first entry)
DE
Factor VIIA (FVIIa) antagonist peptide SEQ ID 41.
KW Antagonist; Factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thromboembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; arteriosclerosis; stenosis; inflammation; septic shock;
KW septicemia; hypotension; angioedema; ARDS.
XX
OS Synthetic.
XX
PN WO200110892-A2.
XX
PD 15-FEB-2001.
XX
PP 04-AUG-2000; 2000WO-US021296.
XX
PR 06-AUG-1999; 99US-0147627P.
XX PR 23-AUG-1999; 99US-0150315P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Dennis MS;
XX
DR WPI; 2001-211069/21.
XX
PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods; inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.
XX
PS Example 1; Fig 4; 80pp; English.
XX
CC This invention relates to peptides which act as antagonist of Factor VIIa
CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
CC activity in the presence of a tissue factor (TF) and for treating a
CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
CC treated include chronic thromboembolic diseases or disorders associated
CC with fibrin formation including vascular disorders such as deep venous
CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
CC arteriosclerosis and restenosis following angioplasty, acute and chronic
CC indications such as inflammation, septic shock, septicaemia, hypotension,
CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
CC and other diseases like inflammatory disorders. The antagonist peptides
CC are also useful in research, and for diagnostic, therapeutic and
CC prophylactic purposes. The present sequence represents a factor VIIa
CC antagonist peptide of the invention
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 WEVLCTWTWETCER 13
| | | | | | | | | |
DB 3 WEVLCTWTWETCER 15
RESULT 20
ID AAB90169 standard; peptide; 24 AA.
XX
AC AAB90169;
XX

```

DT	23-MAY-2001	(first entry)
XX		
DE	Factor VIIa (FVIIa) antagonist peptide SEQ ID 27.	
XX		
KW	Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;	
KM	chronic thromboembolic disease; fibrin formation; vascular disorder;	
KM	deep vein thrombosis; arterial thrombosis; stroke; metastasis;	
KX	thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;	
KW	septicaemia; hypotension; angioedema; ARDS.	
XX		
OS	Synthetic.	
PN	WO200110892-A2.	
XX		
PD	15-FEB-2001.	
XX		
PF	04-AUG-2000; 2000WO-US021296.	
XX		
PR	06-AUG-1999; 99US-0147627P.	
PR	23-AUG-1999; 99US-0150315P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Dennis MS;	
XX		
DR	WPI; 2001-211069/21.	
XX		
PT	New factor VIIa antagonist peptide for research, diagnostic, therapeutic	
PT	and prophylactic methods, inhibits FVII/FVIIa mediated processes and	
PT	blocks initial events of blood coagulation.	
XX		
PS	Example 1; Fig 4; 80pp; English.	
XX		
CC	This invention relates to peptides which act as antagonist of Factor VIIa	
CC	(FVIIa). FVIIa is a trypsin-like serine protease blood coagulation	
CC	factor. FVIIa antagonist peptides are useful for inhibiting FVIIa	
CC	activity in the presence of a tissue factor (TF) and for treating a	
CC	TF/FVIIa mediated disease or disorder in a host. Diseases which can be	
CC	treated include chronic thromboembolic diseases or disorders associated	
CC	with fibrin formation including vascular disorders such as deep venous	
CC	thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,	
CC	arteriosclerosis and restenosis following angioplasty, acute and chronic	
CC	indications such as inflammation, septic shock, septicaemia, hypertension,	
CC	cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory	
CC	distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)	
CC	and other diseases like inflammatory disorders. The antagonist peptides	
CC	are also useful in research, and for diagnostic, therapeutic and	
CC	prophylactic purposes. The present sequence represents a factor VIIa	
CC	antagonist peptide of the invention	
XX		
XX		
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Query Match	100.0%; Score 89; DB 4; Length 24;	
Best Local Similarity	100.0%; Pred. NO. 1.9e-05;	
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db	3 WEVLCTWETCER 15	
RESULT 21		
AAB90168		
ID	AAB90168 standard; peptide; 24 AA.	
AC	AAB90168;	
XX		
XX		
DT	23-MAY-2001 (first entry)	
XX		
DE	Factor VIIa (FVIIa) antagonist peptide SEQ ID 26.	
XX		
XX	Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;	
KW	chronic thromboembolic disease; fibrin formation; vascular disorder;	

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OM protein - protein search, using sw model1

Run on: August 22, 2005, 14:30:13 ; Search time 160 Seconds
(without alignments)
31.816 Million cell updates/sec

Title: US-10-639-076-4
Perfect score: 89
Sequence: 1 WEVLCTWETCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	13	US-10-639-076-4	Sequence 4, Appl1
2	89	100.0	13	US-10-356-257-40	Sequence 40, Appl1
3	89	100.0	15	US-10-639-076-23	Sequence 23, Appl1
4	89	100.0	15	US-10-356-257-3	Sequence 3, Appl1
5	89	100.0	15	US-10-356-257-4	Sequence 4, Appl1
6	89	100.0	15	US-10-356-257-16	Sequence 16, Appl1
7	89	100.0	15	US-10-356-257-32	Sequence 32, Appl1
8	89	100.0	15	US-10-639-076-17	Sequence 17, Appl1
9	89	100.0	18	US-10-639-076-18	Sequence 18, Appl1
10	89	100.0	22	US-10-639-076-57	Sequence 57, Appl1
11	89	100.0	24	US-10-639-076-19	Sequence 19, Appl1

12	89	100.0	24	US-10-639-076-26	Sequence 26, Appl1
13	89	100.0	24	US-10-639-076-27	Sequence 27, Appl1
14	89	100.0	24	US-10-639-076-39	Sequence 39, Appl1
15	89	100.0	24	US-10-639-076-40	Sequence 40, Appl1
16	89	100.0	24	US-10-639-076-41	Sequence 41, Appl1
17	88	98.9	15	US-10-356-257-17	Sequence 17, Appl1
18	88	98.9	15	US-10-639-076-42	Sequence 42, Appl1
19	87	97.8	15	US-10-356-257-18	Sequence 18, Appl1
20	87	97.8	15	US-10-356-257-19	Sequence 19, Appl1
21	87	97.8	24	US-10-639-076-43	Sequence 43, Appl1
22	87	97.8	24	US-10-639-076-44	Sequence 44, Appl1
23	86	96.6	13	US-10-639-076-5	Sequence 5, Appl1
24	86	96.6	15	US-10-356-257-20	Sequence 20, Appl1
25	86	96.6	15	US-10-356-257-27	Sequence 27, Appl1
26	86	96.6	15	US-10-356-257-28	Sequence 28, Appl1
27	86	96.6	24	US-10-639-076-45	Sequence 45, Appl1
28	86	96.6	24	US-10-639-076-52	Sequence 52, Appl1
29	86	96.6	24	US-10-639-076-53	Sequence 53, Appl1
30	85	95.5	15	US-10-356-257-7	Sequence 7, Appl1
31	85	95.5	24	US-10-639-076-30	Sequence 30, Appl1
32	84	94.4	15	US-10-356-257-8	Sequence 8, Appl1
33	84	94.4	15	US-10-356-257-10	Sequence 10, Appl1
34	84	94.4	15	US-10-356-257-13	Sequence 13, Appl1
35	84	94.4	15	US-10-356-257-15	Sequence 15, Appl1
36	84	94.4	15	US-10-356-257-26	Sequence 26, Appl1
37	84	94.4	15	US-10-356-257-29	Sequence 29, Appl1
38	84	94.4	15	US-10-356-257-30	Sequence 30, Appl1
39	84	94.4	24	US-10-639-076-31	Sequence 31, Appl1
40	84	94.4	24	US-10-639-076-33	Sequence 33, Appl1
41	84	94.4	24	US-10-639-076-36	Sequence 36, Appl1
42	84	94.4	24	US-10-639-076-38	Sequence 38, Appl1
43	84	94.4	24	US-10-639-076-51	Sequence 51, Appl1
44	84	94.4	24	US-10-639-076-54	Sequence 54, Appl1
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ALIGNMENTS

RESULT 1
US-10-639-076-4
; Sequence 4, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OR INVENTION: Fv1ta Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-4

Query Match 100.0%; Score 89; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13
Db 1 WEVLCTWETCER 13

```
RESULT 2
US-10-356-257-40
; Sequence 40, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 40
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-40

Query Match          100.0%; Score 89; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCTWETCER 13
        |||
Db      1 WEVLCTWETCER 13

RESULT 3
US-10-639-076-23
; Sequence 23, Application US/10639076
; Publication No. US2004007547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-23

Query Match          100.0%; Score 89; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCTWETCER 13
        |||
Db      3 WEVLCTWETCER 15

RESULT 4
US-10-356-257-3
; Sequence 3, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
```

```
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-3

Query Match          100.0%; Score 89; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCTWETCER 13
        |||
Db      3 WEVLCTWETCER 15

RESULT 5
US-10-356-257-4
; Sequence 4, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-4

Query Match          100.0%; Score 89; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCTWETCER 13
        |||
Db      3 WEVLCTWETCER 15

RESULT 6
US-10-356-257-16
; Sequence 16, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
```

OTHER INFORMATION: sequence is synthesized
US-10-356-257-16

Query Match 100.0%; Score 89; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13
Db 3 WEVLCTWETCER 15

RESULT 7
US-10-356-257-32
Sequence 32, Application US/10356257
Publication No. US2004008767A1
GENERAL INFORMATION:
APPLICANT: LAZARUS, ROBERT A.
APPLICANT: MAUN, HENRY R.
TITLE OF INVENTION: Fv1a Antagonists
FILE REFERENCE: P1950R1
CURRENT APPLICATION NUMBER: US/10/356,257
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/355,420
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 355
SEQ ID NO 32
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-356-257-32

Query Match 100.0%; Score 89; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13
Db 1 WEVLCTWETCER 13

RESULT 8
US-10-639-076-17
Sequence 17, Application US/10639076
Publication No. US2004007547A1
GENERAL INFORMATION:
APPLICANT: Mark S. Dennis
TITLE OF INVENTION: Fv1a Antagonists
FILE REFERENCE: P1639R1
CURRENT APPLICATION NUMBER: US/10/639,076
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/632,429
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/147,627
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 60/150,315
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 17
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-17

Query Match 100.0%; Score 89; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13

Db 2 WEVLCTWETCER 14

RESULT 9
US-10-639-076-18
Sequence 18, Application US/10639076
Publication No. US2004007547A1
GENERAL INFORMATION:
APPLICANT: Mark S. Dennis
TITLE OF INVENTION: Fv1a Antagonists
FILE REFERENCE: P1639R1
CURRENT APPLICATION NUMBER: US/10/639,076
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/632,429
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/147,627
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 60/150,315
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 18
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-18

Query Match 100.0%; Score 89; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13
Db 3 WEVLCTWETCER 15

RESULT 10
US-10-639-076-57
Sequence 57, Application US/10639076
Publication No. US2004007547A1
GENERAL INFORMATION:
APPLICANT: Mark S. Dennis
TITLE OF INVENTION: Fv1a Antagonists
FILE REFERENCE: P1639R1
CURRENT APPLICATION NUMBER: US/10/639,076
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US/09/632,429
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/147,627
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: US 60/150,315
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 100
SEQ ID NO 57
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-57

Query Match 100.0%; Score 89; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWETCER 13
Db 1 WEVLCTWETCER 13

RESULT 11

US-10-639-076-19
; Sequence 19, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-19

Query Match 100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
Db 3 WEVLCTWETCER 15

RESULT 12
US-10-639-076-26
; Sequence 26, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 26
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-26

Query Match 100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
Db 3 WEVLCTWETCER 15

RESULT 13
US-10-639-076-27
; Sequence 27, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis

; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-27

Query Match 100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
Db 3 WEVLCTWETCER 15

RESULT 14
US-10-639-076-39
; Sequence 39, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 39
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-39

Query Match 100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
Db 3 WEVLCTWETCER 15

RESULT 15
US-10-639-076-40
; Sequence 40, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429

```

; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 40
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-40

```

```

Query Match          100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WEVLQWTWETCER 13
        |||||
Db       3 WEVLQWTWETCER 15

```

```

RESULT 16
US-10-639-076-41
; Sequence 41, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 41
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-41

```

```

Query Match          100.0%; Score 89; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 WEVLQWTWETCER 13
        |||||
Db       3 WEVLQWTWETCER 15

```

Search completed: August 22, 2005, 14:54:40
Job time : 160 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 10:19:45 ; Search time 39 Seconds
(without alignments)
32.072 Million cell updates/sec

Title:	US-10-639-076-4
Perfect score:	89
Sequence:	1 MEVLCTWETCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

```
Database :      PIR_79:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	57.3	292	2	S70117	hypothetical prote
2	49	55.1	395	2	B96610	hypothetical prote
3	46	51.7	427	2	T41257	hypothetical prote
4	46	51.7	1080	2	T19048	probable Pro-X-car
5	46	51.7	1121	2	T21303	hypothetical prote
6	46	51.7	1230	2	S47466	cellulose 1,4-beta
7	44	49.4	203	2	A53294	superoxide dismuta
8	43	48.3	516	2	T10000	cytochrome P450 (C
9	43	48.3	524	2	T09999	cytochrome P450 -
10	43	48.3	524	2	T09944	probable cytochrom
11	42	47.2	347	2	D69373	immunogenic protei
12	42	47.2	475	2	T45766	hypothetical prote
13	42	47.2	501	2	E85025	hypothetical prote
14	42	47.2	569	2	S75169	urease (EC 3.5.1.5
15	42	47.2	731	2	T09172	probable calcium-a
16	41.5	46.6	359	2	A22421	3-dehydroshikimate
17	41.5	46.6	519	2	S36808	methylnonyl-CoA
18	41	46.1	242	2	E71621	ERCC1-like excisio
19	41	46.1	276	2	T47351	hypothetical prote
20	41	46.1	278	2	S48776	hypothetical prote
21	41	46.1	306	2	A75316	hypothetical prote
22	41	46.1	330	2	S08500	QUTG protein - Eme
23	41	46.1	340	2	B31277	hypothetical prote
24	41	46.1	481	2	T10036	hypothetical prote
25	41	46.1	494	2	T16658	hypothetical prote
26	41	46.1	575	2	A96766	unknown protein P2
27	41	46.1	594	2	D71347	conserved hypothet
28	41	46.1	732	2	AD0014	primosomal protein
29	41	46.1	856	2	G96814	hypothetical prote

30	41	46.1	95.1	2	T00260	hypothetical prote
31	41	46.1	1085	2	H82511	hypothetical prote
32	41	46.1	1711	2	T21332	hypothetical prote
33	40.5	45.5	1256	2	T47325	hypothetical prote
34	40.5	44.9	4861	2	S71752	giant protein p619
35	40	44.9	280	2	A70513	hypothetical prote
36	40	44.9	225	2	S46749	hypothetical prote
37	40	44.9	306	2	D87531	glycosyl transfera
38	40	44.9	415	2	T49840	hypothetical prote
39	40	44.9	416	2	G86232	cysteine proteinas
40	40	44.9	741	2	T19963	hypothetical prote
41	40	44.9	614	2	B49555	enhancer of split
42	40	44.9	855	2	T29775	hypothetical prote
43	39.5	44.4	348	2	U05250	dehydroshikimate d
44	39.5	44.4	551	2	D75195	hypothetical prote
45	39	43.8	93	2	AC3330	hypothetical prote
46	39	43.8	286	2	C95847	hypothetical trans
47	39	43.8	301	2	AE3373	transporter, dme f
48	39	43.8	317	2	T49995	cyclin protein-lik
49	39	43.8	333	2	AB3597	galactoside transp
50	39	43.8	340	2	JC7695	G protein-coupled
51	39	43.8	361	2	T20105	hypothetical prote
52	39	43.8	428	2	F85437	hypothetical prote
53	39	43.8	439	2	B87039	patatin-like prote
54	39	43.8	438	2	H87371	conserved hypothet
55	39	43.8	438	2	D70528	hexonate transpo
56	39	43.8	471	2	T15394	hypothetical prote
57	39	43.8	472	2	T41684	hypothetical prote
58	39	43.8	479	2	D86340	probable sterol o-
59	39	43.8	509	2	H90994	protein PD20.30 l
60	39	43.8	509	2	B85840	hypothetical prote
61	39	43.8	519	2	T45764	hypothetical prote
62	39	43.8	581	2	H69452	hypothetical prote
63	39	43.8	779	2	AG1978	hypothetical prote
64	39	43.8	993	2	A36873	protein-tyrosine k
65	39	43.8	1253	2	T46248	hypothetical prote
66	39	43.8	1253	2	T14349	Shc protein - mou
67	39	43.8	1305	2	T00670	probable inositol
68	39	43.8	1607	2	T43112	insulin-like growt
69	39	43.8	1829	2	T34239	hypothetical prote
70	39	43.8	2049	2	T29227	hypothetical prote
71	38.5	43.3	1011	2	T45718	receptor-kinase li
72	38.5	43.3	1737	2	T00209	MEG8 protein - hu
73	38	42.7	104	2	C75046	hypothetical prote
74	38	42.7	111	2	T14306	glycine-rich prote
75	38	42.7	117	2	T49511	hypothetical prote
76	38	42.7	179	2	T02878	hypothetical prote
77	38	42.7	179	2	T02815	probable resistanc
78	38	42.7	179	2	T02890	probable disease r
79	38	42.7	214	1	ASLUG5	probable disease r
80	38	42.7	214	1	ASLUG5	probable disease r
81	38	42.7	214	2	S07989	hypothetical prote
82	38	42.7	214	2	T11561	hypothetical prote
83	38	42.7	215	1	ASLUCW	hypothetical prote
84	38	42.7	215	1	ASLUG2	hypothetical prote
85	38	42.7	215	1	ASLUG2	hypothetical prote
86	38	42.7	215	1	ASLUG5	hypothetical prote
87	38	42.7	215	2	SS1093	hypothetical prote
88	38	42.7	215	2	S12154	hypothetical prote
89	38	42.7	215	2	A86437	hypothetical prote
90	38	42.7	216	2	S08437	hypothetical prote
91	38	42.7	229	1	C45345	hypothetical prote
92	38	42.7	244	2	A75418	phosphoserase-re
93	38	42.7	262	2	C84800	3-oxo-alpha-stea
94	38	42.7	262	2	T22371	hypothetical prote
95	38	42.7	267	2	G84004	hypothetical prote
96	38	42.7	292	2	T45680	hypothetical prote
97	38	42.7	301	2	T29657	hypothetical prote
98	38	42.7	333	1	A28396	prostaglandin-F sy
99	38	42.7	333	1	JH0575	chlorocone reduct
100	38	42.7	333	2	T73674	3alpha-hydroyster
101	38	42.7	333	2	B57407	En/Spm-like transp
102	38	42.7	330	2	E84479	

103	38	42.7	451	2	T33233
104	38	42.7	454	2	T21358
105	38	42.7	468	2	T64182
106	38	42.7	471	1	S62590
107	38	42.7	480	2	C70802
108	38	42.7	487	2	T33341
109	38	42.7	519	2	G84707
110	38	42.7	525	2	T21357
111	38	42.7	532	2	T27235
112	38	42.7	539	2	S53529
113	38	42.7	539	2	AF2456
114	38	42.7	585	2	T47330
115	38	42.7	585	2	S44851
116	38	42.7	649	2	S32858
117	38	42.7	660	2	B81839
118	38	42.7	661	2	T47457
119	38	42.7	661	2	D64137
120	38	42.7	675	2	B81101
121	38	42.7	759	2	G64979
122	38	42.7	807	1	MMAD15
123	38	42.7	851	2	T38497
124	38	42.7	881	2	G95574
125	38	42.7	892	2	S57055
126	38	42.7	915	2	A49874
127	38	42.7	1017	2	S67804
128	38	42.7	1052	2	B49120
129	38	42.7	1063	2	T46284
130	38	42.7	1520	1	TVRPA
131	37.5	42.1	229	2	A69762
132	37.5	42.1	317	2	T51204
133	37.5	42.1	619	2	T27026
134	37.5	42.1	934	1	A34372
135	37	41.6	85	2	A40420
136	37	41.6	154	2	A10072
137	37	41.6	154	2	H98263
138	37	41.6	188	2	S61516
139	37	41.6	213	2	T01464
140	37	41.6	243	2	B84490
141	37	41.6	244	2	S25988
142	37	41.6	252	2	S61515
143	37	41.6	258	2	B84455
144	37	41.6	295	2	G90934
145	37	41.6	295	2	C85783
146	37	41.6	295	2	B64933
147	37	41.6	308	2	AE2359
148	37	41.6	318	2	A12336
149	37	41.6	320	2	T73675
150	37	41.6	323	2	T73676
151	37	41.6	323	2	JCS240
152	37	41.6	323	2	A53436
153	37	41.6	329	2	I53872
154	37	41.6	357	2	T34012
155	37	41.6	371	2	B83900
156	37	41.6	381	2	G75589
157	37	41.6	382	2	H64950
158	37	41.6	382	2	B85801
159	37	41.6	382	2	F90952
160	37	41.6	383	2	AF0745
161	37	41.6	383	2	A55546
162	37	41.6	392	2	A41238
163	37	41.6	424	2	JC7102
164	37	41.6	428	2	JCS834
165	37	41.6	443	2	A54813
166	37	41.6	461	2	T20163
167	37	41.6	480	1	S60381
168	37	41.6	490	2	A46391
169	37	41.6	518	2	T50745
170	37	41.6	526	2	JC4533
171	37	41.6	558	2	T40651
172	37	41.6	567	2	T16105
173	37	41.6	569	2	T22928
174	37	41.6	582	2	T16104
175	37	41.6	609	2	T52524

hypothetical prote
Na+/H+-exchanging
peptidyl-prolyl ci
hypothetical prote
probable MYB fam1
hypothetical prote
monophenol monooxy
hypothetical prote
K12H4.7 protein -
oud protein - Brw
probable transmem
hypothetical prote
beta protein homol
transporter, BCTP
hypothetical prote
late 100K protein
hypothetical prote
probable membrane
metabotropic gluta
LRG1 protein - Yea
protein-tyrosine k
protein-tyrosine k
hypothetical prote
hypothetical prote
hypothetical prote
complement C6 prec
depressant insect
conserved hypothet
hypothetical prote
dihydrodiol dehydr
En/Spm-like transp
hypothetical prote
dihydrodiol dehydr
Bn/Spm-like transp
probable excinucle
probable excinucle
hypothetical prote
hypothetical prote
hypothetical prote
chlorodecone reduct
chlorodecone reduct
3alpha-hydroxynol
3-alpha-hydroxyste
dihydrodiol dehydr
hypothetical prote
gentiaste 1,2-diox
hypothetical prote
flagellar biosynth
flagellar biosynth
flagellar biosynth
chemoattractant re
histone deacetylase
histone deacetylase
CAM receptor CAR4
hypothetical prote
RPD1 protein homol
CAM receptor subd
phytoene dehydroge
cytochrome P450 4F
pre-mrna splicing
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

176	37	41.6	629	2	C82598
177	37	41.6	642	2	C96777
178	37	41.6	674	2	F82844
179	37	41.6	699	2	A43734
180	37	41.6	751	2	T04430
181	37	41.6	881	2	A97107
182	37	41.6	925	2	T18747
183	37	41.6	1003	2	T13856
184	37	41.6	1140	2	G89113
185	37	41.6	1148	1	J01604
186	37	41.6	1319	2	S55598
187	37	41.6	1322	2	D82685
188	37	41.6	1363	2	T43220
189	36.5	41.0	205	2	T14745
190	36.5	41.0	601	2	JH0170
191	36.5	41.0	601	2	S12004
192	36.5	41.0	1171	2	T12956
193	36.5	41.0	1286	2	A42150
194	36	40.4	61	2	B34123
195	36	40.4	61	2	C59352
196	36	40.4	85	2	A61616
197	36	40.4	97	2	AF3035
198	36	40.4	99	2	E98250
199	36	40.4	112	2	G70624
200	36	40.4	140	2	G90038

ALIGNMENTS

RESULT 1

S70117
hypothetical protein YDR287W - Yeast (Saccharomyces cerevisiae)

N|Alternate names: hypothetical protein D9819.7

C|Species: Saccharomyces cerevisiae

C|Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

A|Accession: S70117

R|Fulton, L.
submitted to the EMBL Data Library, May 1996

A|Description: The sequence of S. cerevisiae cosmid 9819.

A|Reference number: S70114

A|Accession: S70117

A|Molecule type: DNA

A|Residues: 1-292 <FOLD>

A|Cross-references: UNIPROT:Q05533; EMBL:U51031; NID:G1332635; PID:G1332637; GSPDB:GN000C

C|Genetics:

A|Gene: MIPS:YDR287W

A|Cross-references: SGD:S0002695

A|Map position: 4R

C|Superfamily: suppressor protein subB

Query Match 57.3%; Score 51; DB 2; Length 292;
Best local similarity 54.5%; Pred. No. 3,4;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Cy 1 WEVLQWTWETC 11
DB 223 WEGGCMAMDVC 233

RESULT 2

B96610
hypothetical protein T8123.7 [imported] - Arabidopsis thaliana

C|Species: Arabidopsis thaliana (mouse-ear cress)

C|Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

A|Accession: B96610

R|Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huijzar, L.

Nature 408, 816-820, 2000

A|Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

glucose inhibited
F25A4.24 [imported
oligopeptidase A x
probable protein k
hypothetical prote
alanyl-tRNA synthet
probable potassium
kai protein - fru1
protein ZK742.1 [l
M polyprotein prec
tegument protein 0
phosphoribosylform
insulin-like growth
hypothetical prote
octopamine recepto
tyramine receptor
hypothetical prote
P-glycoprotein pgp
depressant insect
depressant insect
conserved hypothet
hypothetical prote
probable ts1560 tr
hypothetical prote

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <STO>
A:Cross-references: UNIPROT:Q9C693; GB:AE05173; NID:G1055660; PIDN:AA628328.1; GSPDB:G
C:Genetics:
A:Gene: T8L23.7
A:Map position: 1

Query Match 55.1%; Score 49; DB 2; Length 395;
Best Local Similarity 54.5%; Pred. No. 8.7;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVLWMTWETC 11
Db 284 WKLISMAWLTTC 294

RESULT 3
T41257
hypothetical protein SPCC285.11 - fission yeast (*Schizosaccharomyces pombe*)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41257
R:Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21981
A:Accession: T41257
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-427 <SSE>
A:Cross-references: UNIPROT:O74498; EMBL:AL031545; PIDN:CAA20850.1; GSPDB:GN00068; SPDB:
A:Experimental source: strain 972h-; cosmid c285
C:Genetics:
A:Gene: SPDB:SPCC285.11
A:Map position: 3
A:Intons: 36/3

Query Match 51.7%; Score 46; DB 2; Length 427;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLCWTWETC 12
Db 178 ILCTWGDVCE 187

RESULT 4
T19048
probable Pro-X carboxypeptidase F23B2.12 - *Caenorhabditis elegans*
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19048; T21307
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19065
A:Accession: T19048
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <WIL>
A:Cross-references: UNIPROT:O01979; EMBL:Z68295; PIDN:CAA92588.1; GSPDB:GN00022; CESP:F2
A:Experimental source: clone C07C7
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19403
A:Accession: T21307
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <W12>

A:Cross-references: EMBL:Z82266; PIDN:CAB05187.1; GSPDB:GN00022; CESP:F23B2.12
A:Experimental source: clone F23B2
C:Genetics:
A:Gene: CESP:F23B2.12
A:Map position: 4
A:Intons: 19/2; 127/2; 287/3; 349/1; 658/2; 916/2
C:Keywords: duplication

Query Match 51.7%; Score 46; DB 2; Length 1080;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCTWMTWETC 11
Db 886 LMTWMTWETC 893

RESULT 5
T21303
hypothetical protein F23B2.11 - *Caenorhabditis elegans*
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21303
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19403
A:Accession: T21303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1121 <WIL>
A:Cross-references: UNIPROT:O02252; EMBL:Z82266; PIDN:CAB05185.1; GSPDB:GN00022; CESP:F2
A:Experimental source: clone F23B2
C:Genetics:
A:Gene: CESP:F23B2.11
A:Map position: 4
A:Intons: 40/2; 170/2; 330/3; 392/1; 701/2; 958/2

Query Match 51.7%; Score 46; DB 2; Length 1121;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCTWMTWETC 11
Db 928 LMTWMTWETC 935

RESULT 6
S47466
cellulose 1,4-beta-cellobiosidase (BC 3.2.1.91) - *Clostridium thermocellum*
C:Species: Clostridium thermocellum
C>Date: 23-Nov-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S47466
R:Zverlov, V.V.
submitted to the EMBL Data Library, August 1994
A:Reference number: S47466
A:Accession: S47466
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1230 <ZVE>
A:Cross-references: UNIPROT:Q59325; EMBL:X80993; NID:G530013; PIDN:CAA56918.1; PID:G53001
F:1169-1192/Domains: Clostridium cellulase repeat homology <CCR2>
F:1201-1224/Domains: Clostridium cellulase repeat homology <CCR1>

Query Match 51.7%; Score 46; DB 2; Length 1230;
Best Local Similarity 63.6%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCTWMTWETC 12
Db 50 EGLCTWMTWETC 60

RESULT 7

A53294

superoxide dismutase (BC 1.15.1.1) (Mn) - Pseudomonas aeruginosa

C/Species: Pseudomonas aeruginosa

C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C/Accession: A53294; J04981

R/Mangold, U.; Eichel, J.; Wodnicki, W.A.; Wozniak, D.J.; Vasil, M.T.; Cohen, M.S.; Ohman, D.E.

J. Bacteriol. 175, 7658-7665, 1993

A/Title: Cloning and characterization of the Pseudomonas aeruginosa *sodA* and *sodB* genes

dismutase activity in alginate-producing bacteria.

A/Reference number: A53294; MUID:94064560; PMID:8244935

A/Accession: A53294

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-203 <HAS>

A/Cross-references: UNIPROT:P53652; GB:L25672

R/Polack, B.; Dacheux, D.; Delic-Attree, I.; Tousseint, B.; Vignats, P.M.

Biochem. Biophys. Res. Commun. 226, 555-560, 1996

A/Title: The Pseudomonas aeruginosa *fumC* and *sodA* genes belong to an iron-responsive operon

A/Reference number: J04981; MUID:96400296; PMID:8806672

A/Accession: J04981

A/Molecule type: DNA

A/Residues: 1-41, 'ALBETPAQVPSILRLAGLP', 66-203 <POL>

A/Cross-references: GB:U72494; NID:91628609; PTD:AA017391.1; PID:91628613

A/Experimental source: strain CHA

C/Genetics:

A/Status: *sodA*; Mn-SOD

C/Complex: homodimer

A/Function: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C/Superfamily: superoxide dismutase (Mn)

C/Keywords: homodimer; manganese; metalloprotein; oxidoreductase

F/27,81,164,168/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.4%; Score 44; DB 2; Length 203;

Best Local Similarity 46.2%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCMTWETCER 13

Db 53 WRVCCGNMLVCR 65

RESULT 8

cytochrome P450 (CYP72C) - Madagascar periwinkle (fragment)

C/Species: Catharanthus roseus (Madagascar periwinkle)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2004

C/Accession: T10000

R/Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-

Plant Sci. 96, 129-136, 1994

A/Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth

A/Reference number: Z16915

A/Accession: T10000

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-516 <MAN>

A/Cross-references: UNIPROT:Q42701; EMBL:L19075; NID:9404689; PID:9404690

A/Experimental source: cv. cp3

C/Genetics:

A/Status: CYP72C

C/Superfamily: cytochrome P450 homology

C/Keywords: heme; iron; metalloprotein

F/318-481/Domain: cytochrome P450 homology <P45>

F/459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 516;

Best Local Similarity 53.8%; Pred. No. 77;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WEVLCMTWETCER 13

Db 14 WRVLDWAMFTPKR 26

RESULT 9

T09999

cytochrome P450 - Madagascar periwinkle

C/Species: Catharanthus roseus (Madagascar periwinkle)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T09999

R/Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck-

Plant Sci. 96, 129-136, 1994

A/Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharanth

A/Reference number: Z16915

A/Accession: T09999

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-524 <MAN>

A/Cross-references: UNIPROT:Q42700; EMBL:L19074; NID:9404687; PID:9404688

A/Experimental source: cv. cp3

C/Genetics:

A/Status: CYP72B

A/Introns: 96/1; 170/3; 252/2; 381/3

C/Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C/Keywords: heme; iron; metalloprotein

F/329-492/Domain: cytochrome P450 homology <P45>

F/470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 524;

Best Local Similarity 53.8%; Pred. No. 78;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WEVLCMTWETCER 13

Db 25 WRVLDWAMFTPKR 37

RESULT 10

T09944

probable cytochrome P450 protein - Madagascar periwinkle

N/Alternate names: CYP72 protein

C/Species: Catharanthus roseus (Madagascar periwinkle)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T09944

R/Vetter, H.P.; Mangold, U.; Schroeder, G.; Marner, F.J.; Werck-Reichhart, D.; Schroeder,

Plant Physiol. 100, 998-1007, 1992

A/Title: Molecular analysis and heterologous expression of an inducible cytochrome P-450

A/Reference number: Z16902

A/Accession: T09944

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-524 <VERT>

A/Cross-references: UNIPROT:Q05047; EMBL:L10081; NID:9167483; PID:9167484

C/Genetics:

A/Status: CYP72

C/Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology

C/Keywords: heme; iron; metalloprotein

F/329-492/Domain: cytochrome P450 homology <P45>

F/470/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 524;

Best Local Similarity 53.8%; Pred. No. 78;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WEVLCMTWETCER 13

Db 25 WRVLDWAMFTPKR 37

RESULT 11

D69373

immunogenic protein (bcep31-3) homolog - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: D69373

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 A.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Usterbach, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaime, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: D69373
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-347 <KLE>
 A;Cross-references: UNIPROT:O29274; GB:AE001036; GB:AE000782; NID:g2689359; PIDN:AAB9025
 C;Superfamily: immunogenic protein BCSP31

Query Match 47.2%; Score 42; DB 2; Length 347;
 Best Local Similarity 54.5%; Pred. No. 75;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EVLCWETCER 12
 Db 35 EVKPMWATCD 45

RESULT 12
 T45766
 hypothetical protein F24M12.390 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C;Accession: T45766
 R;Vitala, D.; Liqiori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: Z23012
 A;Accession: T45766
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-475 <VIT>
 A;Cross-references: UNIPROT:Q9SD14; EMBL:AL132980
 C;Genetics:
 A;Map position: 3
 A;Intons: 100/2; 147/3; 225/2; 302/2; 319/2; 356/3; 375/3; 399/1
 A;Note: F24M12.390
 C;Superfamily: Arabidopsis thaliana hypothetical protein F24M12.380

Query Match 47.2%; Score 42; DB 2; Length 475;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VLICWTWETCER 12
 Db 15 VVCMGFERCE 24

RESULT 13
 B85025
 hypothetical protein Atg4g01990 (imported) - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: B85025
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488; PMID:10617198
 A;Accession: B85025
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-501 <STO>
 A;Cross-references: UNIPROT:Q9SYJ6; GB:NC_001268; NID:g2768583; PIDN:CAB80692.1; GSPDB:C
 C;Genetics:
 A;Gene: Atg4g01990
 A;Map position: 4

Query Match 47.2%; Score 42; DB 2; Length 501;
 Best Local Similarity 55.6%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 9
 Db 341 WESTCWTYD 349

RESULT 14
 S75169
 urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
 N;Alternate names: protein sll1750
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S75169
 R;Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 sp.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S75169
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-569 <KAN>
 A;Cross-references: UNIPROT:P73061; EMBL:D90903; GB:AB001333; NID:g1652127; PIDN:BA11708;
 C;Genetics:
 A;Gene: ureC
 C;Superfamily: urease, alpha subunit; urease 62K chain homology
 C;Keywords: hydrolase; 62K chain homology <U62>
 P;5-552/Domain: urease 62K chain homology <U62>
 F;136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 47.2%; Score 42; DB 2; Length 569;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EVLCWETCER 13
 Db 371 EVICRTGTATHK 382

RESULT 15
 T09172
 probable calcium-activated potassium channel KCNN3 - human
 C;Species: Homo sapiens (man)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T09172
 R;Chandy, K.G.; Fanning, E.; Wittekandt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman, G.
 Mol. Psychiatry 3, 32-37, 1998
 A;Title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic CAG
 A;Reference number: Z16601; MUID:98150774; PMID:9491810
 A;Accession: T09172
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-731 <CHA>
 A;Cross-references: UNIPROT:Q96DU3; EMBL:AF031815; NID:g3309530; PID:g3309531
 C;Genetics:
 A;Gene: KCNN3
 C;Keywords: potassium channel; schizophrenia

Query Match 47.2%; Score 42; DB 2; Length 731;
 Best Local Similarity 46.2%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWETCER 13
 Db 471 WIIAWTVRACER 483

Mon Aug 22 15:21:10 2005

us-10-639-076-4.rpr

Page 6

Search completed: August 22, 2005, 10:29:51
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 10:18:55 / Search time 168 seconds
(without alignments)
39.625 Million cell updates/sec

Title: US-10-639-076-4
Perfect score: 89
Sequence: 1 MEVLCTWETCER 13

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	58.4	1858	2 Q91PR6	Q91PR6 equaash mola
2	51	57.3	260	2 Q6CAB0	Q6CAB0 yarrowia li
3	51	57.3	292	2 Q05533	Q05533 saccharomyc
4	51	57.3	295	2 Q6PFR7	Q6PFR7 candida gla
5	49	55.1	395	2 Q9C653	Q9C653 arabidopsis
6	49	55.1	533	2 Q8RY80	Q8RY80 arabidopsis
7	48	53.9	460	2 Q8C8K5	Q8C8K5 mus musculu
8	47	52.8	138	2 Q8CAZ0	Q8CAZ0 mus musculu
9	47	52.8	236	2 P79899	P79899 oncorhynch
10	47	52.8	236	2 P79905	P79905 salmo salar
11	47	52.8	1026	2 Q7S2U5	Q7S2U5 neurospora
12	46	51.7	173	2 Q8QLJ0	Q8QLJ0 mamestra co
13	46	51.7	175	2 Q8JMB3	Q8JMB3 mamestra co
14	46	51.7	232	2 Q7IAG8	Q7IAG8 mamestra co
15	46	51.7	315	2 Q7B3G3	Q7B3G3 clostridium
16	46	51.7	427	2 Q74498	Q74498 schistosom
17	46	51.7	1042	2 Q9GRV9	Q9GRV9 caenorhabdi
18	46	51.7	1080	2 Q01979	Q01979 caenorhabdi
19	46	51.7	1121	2 Q02252	Q02252 caenorhabdi
20	46	51.7	1230	2 Q59325	Q59325 clostridium
21	45.5	51.1	807	2 Q86P30	Q86P30 dirosophila
22	45.5	51.1	807	2 Q9V995	Q9V995 dirosophila
23	45	50.6	126	2 Q8N8D9	Q8N8D9 homo sapien
24	45	50.6	426	2 Q87830	Q87830 streptomyce
25	45	50.6	674	2 Q8A282	Q8A282 bacteroides
26	45	50.6	895	2 Q68438	Q68438 clostridium
27	44	49.4	155	2 Q8TMM4	Q8TMM4 methanosarc
28	44	49.4	168	2 Q9DP06	Q9DP06 gilllichthys
29	44	49.4	320	2 Q7VRB2	Q7VRB2 candidatus
30	44	49.4	350	2 Q8TVT5	Q8TVT5 methanopyru
31	43.5	48.9	239	2 Q6Q6F7	Q6Q6F7 burkholderi

32	43.5	48.9	239	2 Q6UBQ1	Q6UBQ1 burkholderi
33	43.5	48.9	239	2 Q6ZBG7	Q6ZBG7 burkholderi
34	43.5	48.9	239	2 Q631X5	Q631X5 burkholderi
35	43	48.3	187	2 Q850L0	Q850L0 pseudosoch
36	43	48.3	205	2 Q96T57	Q96T57 homo sapien
37	43	48.3	361	1 ALR_CORGL	ALR_CORGL corynebacte
38	43	48.3	394	2 Q8TIA3	Q8TIA3 trypanosoma
39	43	48.3	516	2 Q42701	Q42701 catharanthu
40	43	48.3	524	1 CP72_CATRO	CP72_CATRO catharanthu
41	43	48.3	524	2 Q42700	Q42700 catharanthu
42	43	48.3	536	1 KCN1_RAT	KCN1_RAT rattus norv
43	43	48.3	560	1 KCN1_MOUSE	KCN1_MOUSE rattus norv
44	43	48.3	605	2 Q7SAU4	Q7SAU4 neurospora
45	43	48.3	605	2 Q6DE64	Q6DE64 xenopus lae
46	42.5	47.8	88	2 Q816X3	Q816X3 beta coroll
47	42.5	47.8	239	2 Q93NN8	Q93NN8 burkholderi
48	42.5	47.8	239	2 Q93PP4	Q93PP4 burkholderi
49	42.5	47.8	239	2 Q93PP6	Q93PP6 burkholderi
50	42.5	47.8	239	2 Q93PP7	Q93PP7 burkholderi
51	42.5	47.8	239	2 Q93PP9	Q93PP9 burkholderi
52	42.5	47.8	239	2 Q9AM46	Q9AM46 burkholderi
53	42.5	47.8	239	2 Q9AM47	Q9AM47 burkholderi
54	42.5	47.8	239	2 Q9AM48	Q9AM48 burkholderi
55	42.5	47.8	239	2 Q9AM49	Q9AM49 burkholderi
56	42.5	47.8	239	2 Q9AM50	Q9AM50 burkholderi
57	42.5	47.8	239	2 Q9AM51	Q9AM51 burkholderi
58	42.5	47.8	239	2 Q9ZIU0	Q9ZIU0 burkholderi
59	42.5	47.8	450	2 Q8X0H9	Q8X0H9 mus musculu
60	42.5	47.8	591	2 Q6PKX4	Q6PKX4 candida gla
61	42.5	47.8	844	2 Q7ISG9	Q7ISG9 mus musculu
62	42.5	47.8	1315	2 Q7LIJF2	Q7LIJF2 mus musculu
63	42.5	47.8	1405	2 Q8VHS2	Q8VHS2 mus musculu
64	42	47.2	81	2 Q8BXG3	Q8BXG3 photobacter
65	42	47.2	167	2 Q8BXG2	Q8BXG2 mus musculu
66	42	47.2	245	2 Q7SMB5	Q7SMB5 bos taurus
67	42	47.2	253	2 Q67R33	Q67R33 symbiodacte
68	42	47.2	268	2 Q7NCK5	Q7NCK5 gloeobacter
69	42	47.2	325	2 Q6D712	Q6D712 erwilia car
70	42	47.2	333	2 Q6ZVD3	Q6ZVD3 homo sapien
71	42	47.2	347	2 Q29274	Q29274 archaeglob
72	42	47.2	358	2 Q9SBS0	Q9SBS0 medicago va
73	42	47.2	418	2 Q86VP9	Q86VP9 homo sapien
74	42	47.2	426	2 Q8WXG7	Q8WXG7 homo sapien
75	42	47.2	432	2 Q8OX11	Q8OX11 mus musculu
76	42	47.2	439	2 Q8BPH2	Q8BPH2 mus musculu
77	42	47.2	475	2 Q9SD14	Q9SD14 arabidopsis
78	42	47.2	501	2 Q9SYU6	Q9SYU6 arabidopsis
79	42	47.2	502	2 Q93WC5	Q93WC5 arabidopsis
80	42	47.2	543	2 Q6DJU4	Q6DJU4 homo sapien
81	42	47.2	545	2 Q90ZP5	Q90ZP5 oncorhynch
82	42	47.2	553	2 Q9PT89	Q9PT89 gallus gall
83	42	47.2	551	1 KCN1_HUMAN	KCN1_HUMAN homo sapien
84	42	47.2	564	1 Q8CTF3	Q8CTF3 mus musculu
85	42	47.2	569	1 URE1_SYNY3	URE1_SYNY3 synechocyst
86	42	47.2	574	1 KCN2_MOUSE	KCN2_MOUSE mus musculu
87	42	47.2	579	1 KCN2_HUMAN	KCN2_HUMAN homo sapien
88	42	47.2	580	1 KCN2_RAT	KCN2_RAT rattus norv
89	42	47.2	580	1 Q6XVY2	Q6XVY2 homo sapien
90	42	47.2	581	2 Q76C08	Q76C08 bos taurus
91	42	47.2	584	2 Q76C07	Q76C07 bos taurus
92	42	47.2	628	2 Q7S409	Q7S409 neurospora
93	42	47.2	649	2 Q8CAD4	Q8CAD4 mus musculu
94	42	47.2	716	2 Q948Z6	Q948Z6 solanum tub
95	42	47.2	724	1 KCN3_PIG	KCN3_PIG sus scrofa
96	42	47.2	731	1 KCN3_MOUSE	KCN3_MOUSE mus musculu
97	42	47.2	732	1 KCN3_RAT	KCN3_RAT rattus norv
98	42	47.2	736	1 KCN3_HUMAN	KCN3_HUMAN homo sapien
99	42	47.2	737	2 Q96DJ3	Q96DJ3 homo sapien
100	42	47.2	737	2 Q6UXY2	Q6UXY2 homo sapien
101	42	47.2	752	2 Q90ZP4	Q90ZP4 oncorhynch
102	42	47.2	834	2 Q93W18	Q93W18 solanum tub
103	42	47.2	834	2 Q93X19	Q93X19 solanum tub
104	42	47.2	841	2 Q8CCH4	Q8CCH4 mus musculu

Q6UBQ1	burkholderi
Q6ZBG7	burkholderi
Q631X5	burkholderi
Q850L0	pseudosoch
Q96T57	homo sapien
ALR_CORGL	corynebacte
Q8TIA3	trypanosoma
Q42701	catharanthu
CP72_CATRO	catharanthu
Q42700	catharanthu
KCN1_RAT	rattus norv
KCN1_MOUSE	rattus norv
Q7SAU4	neurospora
Q6DE64	xenopus lae
Q816X3	beta coroll
Q93NN8	burkholderi
Q93PP4	burkholderi
Q93PP6	burkholderi
Q93PP7	burkholderi
Q93PP9	burkholderi
Q9AM46	burkholderi
Q9AM47	burkholderi
Q9AM48	burkholderi
Q9AM49	burkholderi
Q9AM50	burkholderi
Q9AM51	burkholderi
Q9ZIU0	burkholderi
Q8X0H9	mus musculu
Q6PKX4	candida gla
Q7ISG9	mus musculu
Q7LIJF2	mus musculu
Q8VHS2	mus musculu
Q8BXG3	photobacter
Q8BXG2	mus musculu
Q7SMB5	bos taurus
Q67R33	symbiodacte
Q7NCK5	gloeobacter
Q6D712	erwilia car
Q6ZVD3	homo sapien
Q29274	archaeglob
Q9SBS0	medicago va
Q86VP9	homo sapien
Q8WXG7	homo sapien
Q8OX11	mus musculu
Q8BPH2	mus musculu
Q9SD14	arabidopsis
Q9SYU6	arabidopsis
Q93WC5	arabidopsis
Q6DJU4	homo sapien
Q90ZP5	oncorhynch
Q9PT89	gallus gall
Q92952	homo sapien
Q8CTF3	mus musculu
P730E1	synechocyst
P5830	mus musculu
P58261	homo sapien
P70604	rattus norv
Q6XVY2	homo sapien
Q76608	bos taurus
Q76607	bos taurus
Q7S409	neurospora
Q8CAD4	mus musculu
Q948Z6	solanum tub
P58392	sus scrofa
P58391	mus musculu
F70605	rattus norv
Q9UG16	homo sapien
Q96DJ3	homo sapien
Q6UXY2	homo sapien
Q90ZP4	oncorhynch
Q93W18	solanum tub
Q93X19	solanum tub
Q8CCH4	mus musculu

105	41.5	46.6	355	2	QBHZN6	QBHzn6 pongo pygma
106	41.5	46.6	359	1	3SHD_NEUCR	P07046 neurospora
107	41.5	46.6	505	2	Q70AC7	Q70ac7 propionibac
108	41.5	46.6	519	2	Q05618	Q05618 propionibac
109	41	46.1	115	2	Q6MYD8	Q6myd8 aspergillus
110	41	46.1	117	2	Q6IVD7	Q6ivd7 strongyloce
111	41	46.1	129	2	Q656W8	Q656w8 oryza sativ
112	41	46.1	183	2	Q7PNS9	Q7pns9 anopheles g
113	41	46.1	196	2	Q7PHR6	Q7phr6 anopheles g
114	41	46.1	200	2	Q6ZA92	Q6za92 oryza sativ
115	41	46.1	236	1	SLR1_RALSO	P58590 ralbionia s
116	41	46.1	236	1	SLR2_RALSO	Q30919 ralbionia s
117	41	46.1	240	2	Q9SDH7	Q9sdh7 oryza sativ
118	41	46.1	241	2	Q9JBA4	Q9jba4 spodioptera
119	41	46.1	242	2	Q96136	Q96136 plasmodium
120	41	46.1	256	2	Q8LR19	Q8lr19 oryza sativ
121	41	46.1	276	2	Q9N1L2	Q9n1l2 arabidopsis
122	41	46.1	278	1	RRP1_YEAST	P35178 saccharomyc
123	41	46.1	285	2	Q8IS28	Q8is28 drosophila
124	41	46.1	285	2	Q8IS29	Q8is29 drosophila
125	41	46.1	294	2	Q72JY9	Q72jk9 thermus the
126	41	46.1	306	2	Q9BSM5	Q9bms deinococcus
127	41	46.1	312	2	Q6BL69	Q6bl69 debaryomyce
128	41	46.1	316	2	Q9AEF9	Q9aei9 jaanthinobac
129	41	46.1	323	2	Q9N4Y6	Q9n4y6 caenorhabdi
130	41	46.1	330	1	OUTG_EMENI	P25416 emericeella
131	41	46.1	331	2	Q6MYX4	Q6myx4 aspergillus
132	41	46.1	335	2	Q6EZM2	Q6ezm2 podospora a
133	41	46.1	340	1	QAK_NEUCR	P11634 neurospora
134	41	46.1	348	2	Q9ST57	Q9st57 drosophila
135	41	46.1	361	2	Q6M9Z6	Q6m9z6 paracanthamyd
136	41	46.1	371	2	Q6FDF3	Q6fdf3 acinetobact
137	41	46.1	397	2	Q7WAI2	Q7wai2 bordetella
138	41	46.1	397	2	Q7WJW9	Q7wjw9 bordetella
139	41	46.1	416	1	PXN1_XENIA	P43263 xenopus lae
140	41	46.1	437	2	Q9ITM5	Q9itm5 lupulid her
141	41	46.1	449	2	Q96UK4	Q96uk4 coccioidoe
142	41	46.1	481	2	Q33088	Q33088 mycobacteri
143	41	46.1	494	2	Q21652	Q21652 caenorhabdi
144	41	46.1	497	2	Q7SKY5	Q7sky5 oryza sativ
145	41	46.1	502	2	Q688G5	Q688g5 oryza sativ
146	41	46.1	519	2	Q81RR8	Q81rr8 drosophila
147	41	46.1	522	2	Q8MRM1	Q8mrml drosophila
148	41	46.1	530	2	Q6EPA9	Q6epa9 oryza sativ
149	41	46.1	559	2	Q6N1O3	Q6n1o3 arabidopsis
150	41	46.1	563	2	Q6CN14	Q6cn14 homo sapien
151	41	46.1	573	2	Q9W4C6	Q9w4c6 drosophila
152	41	46.1	575	2	Q9C9A7	Q9c9a7 arabidopsis
153	41	46.1	594	2	Q83287	Q83287 treponema p
154	41	46.1	608	2	Q6NFE6	Q6nfe6 corynebacte
155	41	46.1	615	2	Q79VE0	Q79ve0 corynebacte
156	41	46.1	615	2	Q8FNC7	Q8fnc7 corynebacte
157	41	46.1	651	2	Q9C9S7	Q9c9s7 arabidopsis
158	41	46.1	678	2	Q8BLF3	Q8blf3 mus musculu
159	41	46.1	695	2	Q7XNM7	Q7xnm7 oryza sativ
160	41	46.1	706	2	Q8XZ11	Q8xz11 ralbionia s
161	41	46.1	732	2	Q66G81	Q66g81 yersinia ps
162	41	46.1	732	2	Q8ZJ11	Q8zj11 yersinia pe
163	41	46.1	791	2	Q810H1	Q810h1 drosophila
164	41	46.1	809	1	WSCK_DROME	P83097 drosophila
165	41	46.1	858	2	Q9W4C7	Q9w4c7 drosophila
166	41	46.1	866	2	Q9SYM1	Q9sym1 arabidopsis
167	41	46.1	886	2	Q7MZM7	Q7mzm7 photorhabdus
168	41	46.1	924	2	Q7KWM5	Q7kwm5 drosophila
169	41	46.1	924	2	Q7KWM6	Q7kwm6 drosophila
170	41	46.1	951	2	Q86TH1	Q86th1 homo sapien
171	41	46.1	1031	2	Q6O345	Q6o345 homo sapien
172	41	46.1	1085	2	Q9KNB5	Q9knb5 vibrio chol
173	41	46.1	1146	2	Q882T7	Q882t7 pseudomonas
174	41	46.1	1514	2	Q7XMR4	Q7xmr4 oryza sativ
175	41	46.1	1591	2	Q45409	Q45409 caenorhabdi
176	41	46.1	1693	2	Q952U8	Q952u8 caenorhabdi
177	41	46.1	2266	2	Q6BBR5	Q6bers caenorhabdi

178	40.5	45.5	488	2	Q951P8	Q951p8 macaca fasc
179	40.5	45.5	493	2	Q6NIM9	Q6nim9 corynebacte
180	40.5	45.5	497	2	Q6A690	Q6a690 propionibac
181	40.5	45.5	610	2	Q6BWU9	Q6bwu9 debaryomyce
182	40.5	45.5	999	2	Q8BR49	Q8br49 m mus muscu
183	40.5	45.5	1256	2	Q9W297	Q9w297 arabidopsis
184	40.5	45.5	1481	2	Q15751	Q15751 homo sapien
185	40.5	44.9	114	2	Q8CBN6	Q8cbn6 mus musculu
186	40.5	44.9	128	2	Q6ZMD3	Q6zmd3 homo sapien
187	40.5	44.9	140	2	Q6G351	Q6g351 staphylococc
188	40.5	44.9	154	2	Q98H58	Q98h58 rhizobium 1
189	40.5	44.9	220	2	Q8L436	Q8l436 hordeum vul
190	40.5	44.9	251	1	SFSA_PROMM	Q7v4t9 prochloroco
191	40.5	44.9	253	2	Q9A618	Q9a618 bacteroides
192	40.5	44.9	254	1	SFSA_SYNFX	Q7u9k2 synechococc
193	40.5	44.9	258	2	Q8AXR5	Q8axr5 brachydanio
194	40.5	44.9	259	2	Q8SUC2	Q8suc2 encephalito
195	40.5	44.9	259	2	Q7VZU3	Q7vzu3 bordetella
196	40.5	44.9	259	2	Q7W567	Q7w567 bordetella
197	40.5	44.9	259	2	Q7WC97	Q7wc97 bordetella
198	40.5	44.9	265	2	Q8IUS6	Q8ius6 homo sapien
199	40.5	44.9	280	2	Q33253	Q33253 mycobacteri
200	40.5	44.9	280	2	Q7T208	Q7t208 mycobacteri

ALIGNMENTS

RESULT 1

Q91PR6 ID Q91PR6 PRELIMINARY; PRT; 1858 AA.

AC Q91PR6; 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

SEQUENCE 1858 AA; 209972 MW; B344D1FC83641829 CRC64;

Query Match 58.4%; Score 52; DB 2; Length 1858;

Best local Similarity 66.7%; Pred. No. 68;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTE 9
Db 1033 WDFCWMWE 1041

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RESULT 2
06CAB0 PRELIMINARY; PRT; 260 AA.
AC 06CAB0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Similar to tr|Q05533 Saccharomyces cerevisiae YDR287W (Fragment).
GN ORFNames=YAL10D04378g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Boismé A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Faithhead C., Ferry-Dumazet H., Giropi A.,
RA Hantaye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Micaud J.M., Nikoleki M., Oztes S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Jouvet M., Wescho E., Wirth B.,
RA Zeniou-Meyer M., Zivancovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in Yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA EMBL: CR182130; CAG80590.1; -
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR CO: GO:0004437; P:inositol or phosphatidylinositol phosphates. . .; IEA.
DR InterPro: IPR000760; Inositol_P.
DR Pfam: PF00459; Inositol_P.1.
DR PRINTS: PR00378; INOSPHPTASE.
DR ProDom: PD023420; Inositol_P.1.
DR PROSITE: PS00629; IMP_1; 1.
DR PROSITE: PS00630; IMP_2; 1.
DR NON_TER 1
SQ SEQUENCE 260 AA; 27973 MW; 8891B53F0AD39337 CRC64;

Query Match 57.3%; Score 51; DB 2; Length 260;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWETC 11
Db 190 WEGGCWAMDVC 200

RESULT 3
Q05533 PRELIMINARY; PRT; 292 AA.
ID Q05533;
AC Q05533;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Ydr287W (YDR287W).
GN ORFNames=YDR287W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=S288C;
RA Fulton L.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kireten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Tach A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Martschky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
RA Hu Y., Vandenberg F., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51031; AAB64472.1; -.
DR EMBL: AY557746; AAS56072.1; -.
DR PIR: S70117; S70117.
DR HSP: P29218; 1IMF.
DR SGD: S00002695; YDR287W.
DR GO: GO:0008934; P:inositol-1(or 4)-monophosphatase activity; IDA.
DR InterPro: IPR00760; Inositol_P.
DR Pfam: PF00459; Inositol_P.1.
DR PRINTS: PR00378; INOSPHPTASE.
DR ProDom: PD023420; Inositol_P.1.
DR PROSITE: PS00629; IMP_1; 1.
DR PROSITE: PS00630; IMP_2; 1.
SQ SEQUENCE 292 AA; 32092 MW; CEA9D943F6E2082 CRC64;

Query Match 57.3%; Score 51; DB 2; Length 292;
Best Local Similarity 54.5%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWETC 11
Db 223 WEGGCWAMDVC 233

RESULT 4
Q6FSE7 PRELIMINARY; PRT; 295 AA.
ID Q6FSE7;
AC Q6FSE7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Similar to tr|Q05533 Saccharomyces cerevisiae YDR287W.
GN ORFNames=CAG10H01089g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Boismé A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,

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RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hartrave F., Hennequin C., Janiaux N., Joyet P., Kachouri R.,
 RA Kerret A., Koszul R., Lemire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenn S., Peltier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennen D., Tekela F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zentou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 DR EMBL; CR380954; CAG59778.1; -;
 DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphates. . ; ISA.
 DR InterPro; IPR000760; Inositol_P.
 DR Pfam; PF00459; Inositol_P.1.
 DR PRINTS; PR00378; INOSPHBTASE.
 DR PRODOM; PD023420; Inositol_P.1.
 DR PROSITE; PS00629; IMP_1.1.
 DR PROSITE; PS00630; IMP_2; UNKNOWN_1.
 SQ SEQUENCE 295 AA; 32903 MW; 1E1F276A74341397 CRC64;

Query Match 57.3%; Score 51; DB 2; Length 295;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WEVLCTWETC 11
 Db 225 WEGGCMWDVC 235

RESULT 5
 Q9C693 PRELIMINARY; PRT; 395 AA.
 AC Q9C693;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein TBL23.7.
 GN Name=TBL23.7;

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;

RP SEQUENCE FROM N.A.
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
 RA Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utechtack T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Niernan W.C., Frazer C.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC079733; AAG50749.1; -;

DR PIR; B96610; B96610.
 DR InterPro; IPR004289; MBOAT_fam.
 DR InterPro; IPR001202; WW_Reps_WWP.
 DR Pfam; PF03062; MBOAT_1.

DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 395 AA; 46301 MW; B798F346E3BE62D3 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 395;
 Best Local Similarity 54.5%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCTWETC 11
 Db 284 WKLMSWMLTC 294

RESULT 6
 Q8RY80 PRELIMINARY; PRT; 533 AA.
 AC Q8RY80;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein Atlg57600.
 GN Name=Atlg57600;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxId=3702;

RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.W., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Caminici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamita A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY074538; AAL69506.1; -;

DR InterPro; IPR004299; MBOAT_fam.
 DR InterPro; IPR001202; WW_Reps_WWP.
 DR Pfam; PF03062; MBOAT_1.
 DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 533 AA; 62791 MW; 5C497F542EB9A66 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 533;
 Best Local Similarity 54.5%; Pred. No. 56;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCTWETC 11
 Db 422 WKLMSWMLTC 432

RESULT 7
 Q8C8K5 PRELIMINARY; PRT; 460 AA.
 AC Q8C8K5;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length
 DE enriched library, clone:B830029103 product:hypothetical G-protein beta
 DE WD-40 repeats containing protein, full insert sequence.
 GN Name=Mdr41;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;

RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX Carminci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]

RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RC The FANTOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).


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RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasuwa T.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 WD repeats.
DR EMBL; AK046853; BAC32897.1; -.
DR MGI; MGI:2445123; Wdr41.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00400; WD40_5.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40_6.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Hypothetical protein; Repeat; WD repeat.
SQ
SEQUENCE 460 AA; 51537 MW; 7387EB4FEBD9AF3 CRC64;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=10349636; DOI=10.1016/S0076-6679(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasuwa T.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK037195; BAC29746.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 138 AA; 15270 MW; 175C0698CFBBA926 CRC64;

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RESULT 8
OC O8CAZO PRELIMINARY; PRT; 138 AA.
AC O8CAZO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:A0300809 product:hypothetical protein, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Query Match 52.8%; Score 47; DB 2; Length 138;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 9
ID P79899 PRELIMINARY; PRT; 236 AA.
AC P79899;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pentaxin precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxId=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatic;
RX MEDLINE=97131713; PubMed=8977214;
RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
RA Whitehead A.S.;
RT "Acute phase proteins in Salmonids. Evolutionary analyses and acute
RT phase response.";
RL J. Immunol. 158:384-392(1997).
DR EMBL; X99385; CAA67764.1; -.
DR HSSP; P02743; ISAC.
DR InterPro; IPR008985; Cona_like_lec_g1.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; Pentaxin.1.
DR PRINTS; PR00895; PENTAXIN.
DR ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
KW SIGNAL.
FT CHAIN 1 23 Potential.
FT 24 236 Pentaxin.
SQ SEQUENCE 236 AA; 26835 MW; 7F39A5F559025857 CRC64;

Query Match
Best Local Similarity 52.8%; Score 47; DB 2; Length 236;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCTWMT 10
Db 116 WISICWTWDS 125

RESULT 10
ID P79905 PRELIMINARY; PRT; 236 AA.
AC P79905;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pentaxin precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OC NCBI_TaxId=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatic;
RX MEDLINE=97131713; PubMed=8977214;
RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
RA Whitehead A.S.;
RT "Acute phase proteins in Salmonids. Evolutionary analyses and acute
RT phase response.";
RL J. Immunol. 158:384-392(1997).
DR EMBL; X99386; CAA67765.1; -.
DR HSSP; P02741; ILJ7.
DR InterPro; IPR008985; Cona_like_lec_g1.
DR InterPro; IPR001759; Pentaxin.
DR Pfam; PF00354; Pentaxin; 1.

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DR PRINTS; PR00895; PENTAXIN.
DR ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
KW SIGNAL.
FT CHAIN 1 23 Potential.
FT 24 236 Pentaxin.
SQ SEQUENCE 236 AA; 26786 MW; FA69D8A65A5B9B57 CRC64;

Query Match
Best Local Similarity 52.8%; Score 47; DB 2; Length 236;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCTWMT 10
Db 116 WISICWTWDS 125

RESULT 11
ID Q782U5 PRELIMINARY; PRT; 1026 AA.
AC Q782U5;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU09030.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OC NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Galvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rahman M.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selltremlkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyssejalis M., Mauceli E., Bielke C., Rudd S., Friesman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Bbbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX0100418; EAA29741.1; -.
SQ SEQUENCE 1026 AA; 115083 MW; 47E9028AE5321A7F CRC64;

Query Match
Best Local Similarity 62.5%; Score 47; DB 2; Length 1026;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCTW 8
Db 358 WSVICWEM 365

RESULT 12
ID Q80LJ0 PRELIMINARY; PRT; 173 AA.
AC Q80LJ0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mamestra configurata nucleopolyhedrovirus (MaconPV).

```

OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=191492;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=90/2;
 RX MEDLINE=97163493; PubMed=9010313;
 RA Li S., Erlanson M., Moody D., Gillett C.;
 RT "A physical map of the Mamestra configurata nucleopolyhedrovirus
 genome and sequence analysis of the polyhedrin gene.";
 RL J. Gen. Virol. 78:265-271(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=90/2;
 RX MEDLINE=21864635; PubMed=11886270; DOI=10.1006/viro.2001.1313;
 RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlanson M.;
 RT "Sequence and organization of the Mamestra configurata
 nucleopolyhedrovirus genome.";
 RL Virology 294:106-121(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=90/2;
 RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlanson M.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U59461; AAM09152.1; -;
 DR InterPro; IPR011568; Viral_DUF.
 DR Prodom; PD021627; Viral_DUF; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 173 AA; 20238 MW; F85DFDAA70912360 CRC64;
 QY 3 VLCTWETCER 13
 Db 146 VRCWVGJCEK 156
 Query Match 51.7%; Score 46; DB 2; Length 173;
 Best Local Similarity 54.5%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 13
 ID Q8JMB3 PRELIMINARY; PRT; 175 AA.
 AC Q8JMB3;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Mamestra configurata nucleopolyhedrovirus B.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=204440;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22080411; PubMed=12083822; DOI=10.1006/viro.2002.1411;
 RA Li L., Donly C., Li Q., Willis L.G., Keddie B.A., Erlanson M.A.,
 RT Theilmann D.A.;
 RT "Identification and genomic analysis of a second species of
 nucleopolyhedrovirus isolated from Mamestra configurata.";
 RL Virology 297:226-244(2002).
 DR EMBL; AY126275; AAM95026.1; -;
 DR InterPro; IPR011568; Viral_DUF.
 DR Prodom; PD021627; Viral_DUF; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 175 AA; 20193 MW; 8999CC171B8133C7 CRC64;
 QY 3 VLCTWETCER 13
 Db 148 VRCWVGJCEK 158
 Query Match 51.7%; Score 46; DB 2; Length 175;
 Best Local Similarity 54.5%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 14
 ID Q71AG8 PRELIMINARY; PRT; 232 AA.
 AC Q71AG8;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mamestra configurata nucleopolyhedrovirus A.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=207830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Li L., Li Q., Willis L.G., Erlanson M., Theilmann D.A., Donly C.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF539999; AAQ11063.1; -;
 DR InterPro; IPR011568; Viral_DUF.
 DR Prodom; PD021627; Viral_DUF; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 232 AA; 26958 MW; 9D4302AB6BC39B1B CRC64;
 QY 3 VLCTWETCER 13
 Db 205 VRCWVGJCEK 215
 Query Match 51.7%; Score 46; DB 2; Length 232;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 15
 ID Q7B3G3 PRELIMINARY; PRT; 315 AA.
 AC Q7B3G3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Cellulose 1,4-beta-cellulobiosidase (EC 3.2.1.91) (Fragment).
 GN Name=cba;
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F7;
 RX MEDLINE=99351130; PubMed=10422230;
 RA Zverlov V.V., Velikodvorskaya G.A., Schwarz W.H.;
 RT "Purified Clostridium thermocellum cellobiohydrolase gene encoding
 RT cellulosomal subunits S3 and S.";
 RL Appl. Microbiol. Biotechnol. 51:852-859(1999).
 DR EMBL; AJ005783; CA06693.1; -;
 DR GO; GO:0008810; F:cellulase activity; IEA.
 DR GO; GO:0016162; F:cellulose 1,4-beta-cellulobiosidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR003305; CBM_Cent.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR004197; Glyco_hydro_91g.
 DR Pfam; PF02018; CBM 4.9; 1.
 DR Pfam; PF02927; CeId N; 1.
 KM Glycosidase; Hydrolase.
 FT NON_TER
 SQ SEQUENCE 315 AA; 35887 MW; 55148EC06413ADC0 CRC64;
 QY 2 EVLCWTWETCER 12
 Db 2 EVLCWTWETCER 12
 Query Match 51.7%; Score 46; DB 2; Length 315;
 Best Local Similarity 63.6%; Pred. No. 90;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 50 ECLCPWHTCE 60

Search completed: August 22, 2005, 10:29:10
Job time : 179 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 22, 2005, 10:20:35 ; Search time 42 Seconds
(without alignments)
23.106 Million cell updates/sec

Title: US-10-639-076-4
Perfect score: 89
Sequence: 1 MEVLCTWETCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	47	52.8	54	4	US-09-621-976-5389
2	47	52.8	54	4	US-09-621-976-5390
3	46	51.7	407	4	US-09-252-991A-29811
4	45.5	51.1	126	4	US-09-949-016-10235
5	45.5	51.1	169	4	US-09-270-767-40967
6	45.5	51.1	169	4	US-09-270-767-56183
7	44	49.4	102	4	US-09-702-705-1818
8	44	49.4	102	4	US-09-736-457-1818
9	44	49.4	102	4	US-09-671-325-1818
10	44	49.4	216	4	US-09-252-991A-23048
11	44	49.4	257	4	US-09-252-991A-31868
12	43.5	48.9	13	4	US-10-158-847-101
13	43.5	48.9	21	4	US-10-158-847-30
14	43	48.3	54	3	US-08-851-843A-183
15	43	48.3	54	3	US-08-974-549A-302
16	43	48.3	54	3	US-08-854-050-183
17	43	48.3	54	3	US-09-430-323-183
18	43	48.3	54	4	US-09-402-181B-302
19	43	48.3	54	4	US-09-721-456-302
20	43	48.3	227	4	US-09-252-991A-30379
21	43	48.3	458	4	US-09-922-364A-4
22	43	48.3	458	4	US-09-254-590-4
23	43	48.3	458	4	US-10-115-415-4
24	43	48.3	458	4	US-10-116-260-4
25	43	48.3	458	4	US-10-115-671-4
26	42	47.2	13	4	US-10-158-847-103
27	42	47.2	328	4	US-09-922-364A-27

28	42	47.2	328	4	US-09-254-590-27	Sequence 27, Appl
29	42	47.2	328	4	US-10-115-415-27	Sequence 27, Appl
30	42	47.2	328	4	US-10-116-260-27	Sequence 27, Appl
31	42	47.2	328	4	US-10-115-671-27	Sequence 27, Appl
32	42	47.2	386	4	US-09-949-016-10095	Sequence 10095, A
33	42	47.2	553	4	US-09-922-364A-3	Sequence 3, Appl1
34	42	47.2	553	4	US-09-254-590-3	Sequence 3, Appl1
35	42	47.2	553	4	US-10-115-415-3	Sequence 3, Appl1
36	42	47.2	553	4	US-10-116-260-3	Sequence 3, Appl1
37	42	47.2	553	4	US-10-115-671-3	Sequence 3, Appl1
38	42	47.2	557	4	US-09-922-364A-20	Sequence 20, Appl
39	42	47.2	557	4	US-09-254-590-20	Sequence 20, Appl
40	42	47.2	557	4	US-10-115-415-20	Sequence 20, Appl
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42	42	47.2	557	4	US-10-115-671-20	Sequence 20, Appl
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44	42	47.2	561	4	US-09-254-590-1	Sequence 1, Appl1
45	42	47.2	561	4	US-09-949-016-6197	Sequence 6197, Ap
46	42	47.2	561	4	US-10-115-415-1	Sequence 1, Appl1
47	42	47.2	561	4	US-10-116-260-1	Sequence 1, Appl1
48	42	47.2	561	4	US-10-115-671-1	Sequence 1, Appl1
49	42	47.2	579	4	US-09-922-364A-19	Sequence 19, Appl
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60	42	47.2	712	4	US-09-252-991A-20471	Sequence 20471, A
61	42	47.2	731	3	US-09-115-446-2	Sequence 2, Appl1
62	42	47.2	731	4	US-09-275-252A-10	Sequence 10, Appl
63	42	47.2	731	4	US-09-565-590-2	Sequence 2, Appl1
64	42	47.2	732	4	US-09-922-364A-43	Sequence 43, Appl
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66	42	47.2	732	4	US-10-115-415-43	Sequence 43, Appl
67	42	47.2	732	4	US-10-116-260-43	Sequence 43, Appl
68	42	47.2	732	4	US-10-115-671-43	Sequence 43, Appl
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78	41	46.1	115	4	US-09-621-976-5517	Sequence 5517, Ap
79	41	46.1	172	4	US-09-270-767-60977	Sequence 60977, A
80	41	46.1	202	4	US-09-922-364A-10104	Sequence 20104, A
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82	41	46.1	419	4	US-09-902-540-10098	Sequence 45469, A
83	41	46.1	526	4	US-09-270-767-45469	Sequence 45469, A
84	41	46.1	615	4	US-09-252-991A-23688	Sequence 23688, A
85	41	46.1	615	4	US-09-602-787A-534	Sequence 534, App
86	40.5	45.5	461	4	US-09-602-787A-536	Sequence 536, App
87	40	44.9	90	4	US-09-919-497-70	Sequence 70, Appl
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95	40	44.9	443	3	US-08-922-364A-10	Sequence 65, Appl
96	40	44.9	866	2	US-08-620-694A-10	Sequence 10, Appl
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98	40	44.9	866	3	US-09-022-696-10	Sequence 10, Appl
99	40	44.9	866	3	US-08-978-773-4	Sequence 4, Appl1
100	40	44.9	866	3	US-09-022-255-10	Sequence 10, Appl

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102	40	44.9	866	3	US-09-022-257-10	Sequence 10, Appl	175	38	42.7	262	3	US-08-634-475-2	Sequence 2, Appl
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105	40	44.9	900	3	US-08-890-865A-4	Sequence 4, Appl	178	38	42.7	297	4	US-09-252-991A-28842	Sequence 28842, A
106	40	44.9	1088	4	US-09-949-016-8011	Sequence 8011, Ap	179	38	42.7	323	3	US-08-532-896-2	Sequence 2, Appl
107	39.5	44.4	18	3	US-08-825-852-79	Sequence 79, Appl	180	38	42.7	374	4	US-09-352-991A-19475	Sequence 19475, A
108	39.5	44.4	18	3	US-09-052-888-80	Sequence 80, Appl	181	38	42.7	386	4	US-10-101-464A-902	Sequence 902, Appl
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111	39.5	44.4	18	4	US-09-723-547-80	Sequence 80, Appl	184	38	42.7	481	3	US-09-817-464-8	Sequence 8, Appl
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113	39.5	44.4	18	4	US-09-723-931-80	Sequence 80, Appl	186	38	42.7	867	4	US-09-817-464-4	Sequence 4, Appl
114	39.5	44.4	18	4	US-09-723-873-80	Sequence 80, Appl	187	38	42.7	915	1	US-08-453-862-2	Sequence 2, Appl
115	39.5	44.4	18	4	US-09-724-114-80	Sequence 80, Appl	188	38	42.7	915	2	US-08-452-734A-2	Sequence 2, Appl
116	39.5	44.4	18	4	US-09-723-913-80	Sequence 80, Appl	189	38	42.7	915	3	US-08-617-785-12	Sequence 12, Appl
117	39.5	44.4	18	4	US-09-723-912-80	Sequence 80, Appl	190	38	42.7	915	3	US-08-176-401B-2	Sequence 2, Appl
118	39.5	44.4	18	4	US-09-724-095-80	Sequence 80, Appl	191	38	42.7	915	4	US-09-817-464-12	Sequence 12, Appl
119	39.5	44.4	18	4	US-09-724-157-80	Sequence 80, Appl	192	38	42.7	915	5	PCT-US94-14989-2	Sequence 2, Appl
120	39.5	44.4	18	4	US-09-724-062-80	Sequence 80, Appl	193	38	42.7	922	4	US-08-617-785-14	Sequence 14, Appl
121	39.5	44.4	18	4	US-09-724-065-80	Sequence 80, Appl	194	38	42.7	922	4	US-09-817-464-14	Sequence 14, Appl
122	39.5	44.4	117	4	US-09-270-767-47400	Sequence 47400, A	195	38	42.7	1402	4	US-09-711-619-9	Sequence 9, Appl
123	39.5	44.4	196	4	US-09-252-991A-23657	Sequence 23657, A	196	38	42.7	3077	6	5223423-2	Patent No. 5223423
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125	39.5	44.4	13	4	US-10-158-847-112	Sequence 112, App	198	37.5	42.1	13	4	US-10-158-847-118	Sequence 118, App
126	39	43.8	135	4	US-09-252-991A-24701	Sequence 24701, A	199	37	41.6	33	4	US-08-624-735E-15	Sequence 15, Appl
127	39	43.8	265	4	US-09-949-016-9336	Sequence 9336, Ap	200	37	41.6	33	4	US-08-624-735E-16	Sequence 16, Appl
128	39	43.8	296	4	US-09-328-352-7482	Sequence 7482, Ap							
129	39	43.8	311	4	US-09-488-039A-13013	Sequence 13013, A							
130	39	43.8	323	4	US-09-252-991A-22747	Sequence 22747, A							
131	39	43.8	340	4	US-09-712-368-1	Sequence 1, Appl							
132	39	43.8	341	4	US-09-328-352-6124	Sequence 6124, Ap							
133	39	43.8	361	4	US-09-543-681A-6707	Sequence 6707, Ap							
134	39	43.8	417	4	US-09-252-991A-28413	Sequence 28413, A							
135	39	43.8	429	4	US-08-311-731A-68	Sequence 68, Appl							
136	39	43.8	474	4	US-08-311-731A-518	Sequence 318, App							
137	39	43.8	493	4	US-09-543-681A-4617	Sequence 4617, Ap							
138	39	43.8	504	4	US-09-252-991A-28242	Sequence 28242, A							
139	39	43.8	993	1	US-08-183-211-2	Sequence 2, Appl							
140	39	43.8	993	5	PCT-US95-00176A-2	Sequence 2, Appl							
141	39	43.8	1024	4	US-09-562-737-83	Sequence 83, Appl							
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143	38.5	43.3	488	4	US-09-538-092-1367	Sequence 1367, Ap							
144	38.5	43.3	556	4	US-09-949-016-7424	Sequence 7424, Ap							
145	38	42.7	48	3	US-08-630-916A-72	Sequence 72, Appl							
146	38	42.7	118	4	US-09-513-999C-8155	Sequence 8155, Ap							
147	38	42.7	146	4	US-09-252-991A-17306	Sequence 17306, A							
148	38	42.7	147	4	US-09-248-796A-19986	Sequence 19986, A							
149	38	42.7	152	4	US-09-702-705-787	Sequence 787, App							
150	38	42.7	152	4	US-09-702-705-795	Sequence 795, App							
151	38	42.7	152	4	US-09-736-457-787	Sequence 787, App							
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154	38	42.7	152	4	US-09-614-124B-795	Sequence 795, App							
155	38	42.7	152	4	US-09-671-325-787	Sequence 787, App							
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161	38	42.7	162	4	US-09-252-991A-19256	Sequence 19256, A							
162	38	42.7	179	2	US-08-481-956A-11	Sequence 11, Appl							
163	38	42.7	179	2	US-08-629-291A-11	Sequence 11, Appl							
164	38	42.7	179	2	US-08-658-335B-11	Sequence 11, Appl							
165	38	42.7	179	2	US-09-406-640-11	Sequence 11, Appl							
166	38	42.7	182	4	US-09-252-991A-26845	Sequence 26845, A							
167	38	42.7	187	4	US-10-101-464A-732	Sequence 732, App							
168	38	42.7	215	2	US-08-659-251-8	Sequence 8, Appl							
169	38	42.7	215	2	US-09-256-490-8	Sequence 8, Appl							
170	38	42.7	215	5	PCT-US96-11445-8	Sequence 8, Appl							
171	38	42.7	233	4	US-09-270-767-41694	Sequence 41694, A							
172	38	42.7	246	3	US-08-634-475-3	Sequence 3, Appl							
173	38	42.7	246	3	US-09-709-791-3	Sequence 3, Appl							

174	38	42.7	261	2	US-07-857-224B-60	Sequence 60, Appl
175	38	42.7	262	3	US-08-634-475-2	Sequence 2, Appl
176	38	42.7	262	3	US-09-709-791-2	Sequence 2, Appl
177	38	42.7	283	4	US-09-949-016-7078	Sequence 7078, Ap
178	38	42.7	297	4	US-09-252-991A-28842	Sequence 28842, A
179	38	42.7	323	3	US-08-532-896-2	Sequence 2, Appl
180	38	42.7	374	4	US-09-352-991A-19475	Sequence 19475, A
181	38	42.7	386	4	US-10-101-464A-902	Sequence 902, Appl
182	38	42.7	453	4	US-09-252-991A-24830	Sequence 24830, A
183	38	42.7	481	3	US-08-617-785-8	Sequence 8, Appl
184	38	42.7	481	3	US-09-817-464-8	Sequence 8, Appl
185	38	42.7	867	3	US-08-617-785-4	Sequence 4, Appl
186	38	42.7	867	4	US-09-817-464-4	Sequence 4, Appl
187	38	42.7	915	1	US-08-453-862-2	Sequence 2, Appl
188	38	42.7	915	2	US-08-452-734A-2	Sequence 2, Appl
189	38	42.7	915	3	US-08-617-785-12	Sequence 12, Appl
190	38	42.7	915	3	US-08-176-401B-2	Sequence 2, Appl
191	38	42.7	915	4	US-09-817-464-12	Sequence 12, Appl
192	38	42.7	915	5	PCT-US94-14989-2	Sequence 2, Appl
193	38	42.7	922	4	US-08-617-785-14	Sequence 14, Appl
194	38	42.7	922	4	US-09-817-464-14	Sequence 14, Appl
195	38	42.7	1402	4	US-09-711-619-9	Sequence 9, Appl
196	38	42.7	3077	6	5223423-2	Patent No. 5223423
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198	37.5	42.1	13	4	US-10-158-847-118	Sequence 118, App
199	37	41.6	33	4	US-08-624-735E-15	Sequence 15, Appl
200	37	41.6	33	4	US-08-624-735E-16	Sequence 16, Appl

ALIGNMENTS

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--RESULT 1
US-09-621-976-5389
; Sequence 5389, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 5389
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -47..-1
; NAME/KEY: UNSURE
; LOCATION: 5
; OTHER INFORMATION: Xaa = Phe,Leu
US-09-621-976-5389

Query Match      52.8%; Score 47; DB 4; Length 54;
Best Local Similarity 60.0%; Pred No. 8.6;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Db      41 VLCTWMLSK 50

--RESULT 2
US-09-621-976-5390
; Sequence 5390, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
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RESULT 7

US-09-702-705-1818
; Sequence 1818, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-1818

Query Match 49.4%; Score 44; DB 4; Length 102;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCTWE 9
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Db 55 WRLMCWME 63

RESULT 8
US-09-736-457-1818
; Sequence 1818, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1818

Query Match 49.4%; Score 44; DB 4; Length 102;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCTWE 9
| : ||||
Db 55 WRLMCWME 63

RESULT 9

US-09-671-325-1818
; Sequence 1818, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-1818

Query Match 49.4%; Score 44; DB 4; Length 102;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCTWE 9
| : ||||
Db 55 WRLMCWME 63

RESULT 10
US-09-252-991A-23048
; Sequence 23048, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23048
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23048

Query Match 49.4%; Score 44; DB 4; Length 216;
Best Local Similarity 50.0%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWET 10
| : ||||
Db 97 WDTSCWTWPT 106

RESULT 11
US-09-252-991A-31868
; Sequence 31868, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31868
LENGTH: 257
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31868

Query Match 49.4%; Score 44; DB 4; Length 257;
Best Local Similarity 55.6%; Pred. No. 94;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CMTWETCER 13
DB 236 CMTWETCER 244

RESULT 12
US-10-158-847-101
Sequence 101, Application US/10158847
Patent No. 6592865
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PP557
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,004
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 101
LENGTH: 13
TYPE: PRT
ORGANISM: homo sapiens
US-10-158-847-101

Query Match 48.9%; Score 43.5; DB 4; Length 13;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLWETCER 12
DB 1 W-VLCPEWEDCD 11

RESULT 13
US-10-158-847-30
Sequence 30, Application US/10158847
Patent No. 6592865
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PP557
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,004
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30
LENGTH: 21
TYPE: PRT
ORGANISM: homo sapiens
US-10-158-847-30

Query Match 48.9%; Score 43.5; DB 4; Length 21;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLWETCER 12
DB 3 W-VLCPEWEDCD 13

RESULT 14
US-08-851-843A-183
Sequence 183, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-851-843A-183

Query Match 48.3%; Score 43; DB 3; Length 54;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLWETW 8

Db 18 WAPLCWAW 25

RESULT 15

US-08-974-549A-302
Sequence 302, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Klingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-302

Query Match 48.3%; Score 43; DB 3; Length 54;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVICWTW 8
Db 18 WAPLCWAW 25

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Job time : 44 secs

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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:42:55 ; Search time 191 Seconds
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Title: US-10-639-076-4
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SUMMARIES

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1	89	100.0	13	AA890146	Aab90146 Factor VI
2	89	100.0	13	ABR82342	Abi82342 Factor X
3	89	100.0	13	ADM96618	Adm96618 Tissue fa
4	89	100.0	15	AA890165	Aab90165 Factor VI
5	89	100.0	15	ABR82341	Abi82341 Factor X
6	89	100.0	15	ADM96610	Adm96610 Tissue fa
7	89	100.0	15	ADM96581	Adm96581 Tissue fa
8	89	100.0	15	ADM96582	Adm96582 Tissue fa
9	89	100.0	15	ADM96594	Adm96594 Tissue fa
10	89	100.0	16	AA890159	Aab90159 Factor VI
11	89	100.0	16	ABR82340	Abi82340 Factor X
12	89	100.0	18	AA890160	Aab90160 Factor VI
13	89	100.0	18	ABR82338	Abi82338 Factor X
14	89	100.0	18	ABR82339	Abi82339 Factor X
15	89	100.0	20	ABR82337	Abi82337 Factor X
16	89	100.0	22	AA890159	Aab90159 Factor VI
17	89	100.0	22	AA890182	Aab90182 Factor VI
18	89	100.0	24	AA890181	Aab90181 Factor VI
19	89	100.0	24	AA890183	Aab90183 Factor VI
20	89	100.0	24	AA890189	Aab90189 Factor VI
21	89	100.0	24	AA890168	Aab90168 Factor VI
22	89	100.0	24	AA890161	Aab90161 Factor VI
23	89	98.9	15	ADM96595	Adm96595 Tissue fa
24	88	98.9	24	AA890184	Aab90184 Factor VI

25	87	97.8	15	ADM96596	Adm96596 Tissue fa
26	87	97.8	15	ADM96597	Adm96597 Tissue fa
27	87	97.8	24	AA890185	Aab90185 Factor VI
28	87	97.8	24	AA890186	Aab90186 Factor VI
29	86	96.6	13	AA890147	Aab90147 Factor VI
30	86	96.6	15	ADM96605	Adm96605 Tissue fa
31	86	96.6	15	ADM96598	Adm96598 Tissue fa
32	86	96.6	15	ADM96606	Adm96606 Tissue fa
33	86	96.6	24	AA890194	Aab90194 Factor VI
34	86	96.6	24	AA890187	Aab90187 Factor VI
35	86	96.6	24	AA890195	Aab90195 Factor VI
36	85	95.5	15	ADM96585	Adm96585 Tissue fa
37	85	95.5	15	ADM96591	Adm96591 Tissue fa
38	84	94.4	12	ABR82347	Abi82347 Factor X
39	84	94.4	15	ADM96607	Adm96607 Tissue fa
40	84	94.4	15	ADM96608	Adm96608 Tissue fa
41	84	94.4	15	ADM96592	Adm96592 Tissue fa
42	84	94.4	15	ADM96586	Adm96586 Tissue fa
43	84	94.4	15	ADM96588	Adm96588 Tissue fa
44	84	94.4	15	AA890196	Aab90196 Factor VI
45	84	94.4	24	AA890175	Aab90175 Factor VI
46	84	94.4	24	AA890197	Aab90197 Factor VI
47	84	94.4	24	AA890178	Aab90178 Factor VI
48	84	94.4	24	AA890173	Aab90173 Factor VI
49	84	94.4	24	AA890193	Aab90193 Factor VI
50	84	94.4	24	AA890207	Aab90207 Factor VI
51	84	94.4	24	AA890173	Aab90173 Factor VI
52	84	94.4	24	AA890178	Aab90178 Factor VI
53	84	94.4	13	AA890145	Aab90145 Factor VI
54	83	93.3	15	ADM96590	Adm96590 Tissue fa
55	83	93.3	15	ADM96584	Adm96584 Tissue fa
56	83	93.3	15	ADM96592	Adm96592 Tissue fa
57	83	93.3	15	ADM96585	Adm96585 Tissue fa
58	83	93.3	24	AA890171	Aab90171 Factor VI
59	83	93.3	24	AA890179	Aab90179 Factor VI
60	83	93.3	18	AA890219	Aab90219 Factor VI
61	82	92.1	20	AA890237	Aab90237 Factor VI
62	82	92.1	20	AA890231	Aab90231 Factor VI
63	82	92.1	18	AA890220	Aab90220 Factor VI
64	81	91.0	15	ADM96615	Adm96615 Tissue fa
65	80	89.9	15	ADM96617	Adm96617 Tissue fa
66	80	89.9	15	ADM96616	Adm96616 Tissue fa
67	80	89.9	24	AA890204	Aab90204 Factor VI
68	80	89.9	24	AA890205	Aab90205 Factor VI
69	80	89.9	24	AA890206	Aab90206 Factor VI
70	80	89.9	24	AA890206	Aab90206 Factor VI
71	79	88.8	11	ABR82348	Abi82348 Factor X
72	79	88.8	15	ADM96611	Adm96611 Tissue fa
73	79	88.8	15	ADM96599	Adm96599 Tissue fa
74	79	88.8	15	ADM96602	Adm96602 Tissue fa
75	79	88.8	15	ADM96613	Adm96613 Tissue fa
76	79	88.8	22	AA890202	Aab90202 Factor VI
77	79	88.8	22	AA890202	Aab90202 Factor VI
78	79	88.8	24	AA890191	Aab90191 Factor VI
79	79	88.8	24	AA890188	Aab90188 Factor VI
80	78	87.6	12	ABR82343	Abi82343 Factor X
81	78	87.6	12	ABR82343	Abi82343 Factor X
82	78	87.6	15	ADM96583	Adm96583 Tissue fa
83	78	87.6	15	ADM96583	Adm96583 Tissue fa
84	78	87.6	18	AA890221	Aab90221 Factor VI
85	78	87.6	20	AA890215	Aab90215 Factor VI
86	78	87.6	20	AA890215	Aab90215 Factor VI
87	78	87.6	20	AA890215	Aab90215 Factor VI
88	78	87.6	20	AA890215	Aab90215 Factor VI
89	78	87.6	20	AA890215	Aab90215 Factor VI
90	78	87.6	24	AA890224	Aab90224 Factor VI
91	77	86.5	13	ADM96601	Adm96601 Tissue fa
92	77	86.5	15	ADM96601	Adm96601 Tissue fa
93	77	86.5	15	ADM96601	Adm96601 Tissue fa
94	76	85.4	13	AA890229	Aab90229 Factor VI
95	76	85.4	15	ADM96603	Adm96603 Tissue fa
96	76	85.4	15	ADM96600	Adm96600 Tissue fa
97	76	85.4	18	AA890222	Aab90222 Factor VI

98	76	85.4	20	4	AA90214	Factor VI	171	46	51.7	50	9	AEA30320
99	76	85.4	20	6	ABR82329	Clone AB	172	46	51.7	407	7	ABO81065
100	76	85.4	24	4	AA90192	Factor VI	173	45.5	51.1	122	4	ABG26675
101	76	85.4	24	4	AA90189	Factor VI	174	45.5	50.6	808	4	ABR70322
102	75	84.3	13	4	AA90167	Factor VI	175	45	50.6	37	8	ABO57247
103	75	84.3	15	8	ADM95589	Tissue fa	176	45	50.6	126	7	ADM05346
104	75	84.3	15	8	ADM95587	Tissue fa	177	45	50.6	426	2	AAW9397
105	75	84.3	20	4	AA90236	Factor VI	178	44	49.4	25	4	AAW19888
106	75	84.3	24	4	AA90176	Factor VI	179	44	49.4	25	4	ABR39831
107	75	84.3	24	4	AA90174	Factor VI	180	44	49.4	25	4	ABR24435
108	74	83.1	20	4	AA90212	Factor VI	181	44	49.4	25	4	AAW73218
109	74	83.1	20	6	ABR82327	Clone AC	182	44	49.4	25	4	AAW73218
110	73	82.0	11	6	ABR82344	Factor X	183	44	49.4	25	4	ABG54934
111	73	82.0	12	4	AA90151	Factor VI	184	44	49.4	25	4	ABG43065
112	73	82.0	13	4	AA90227	Factor VI	185	44	49.4	25	8	ABO60599
113	73	82.0	13	4	AA90150	Factor VI	186	44	49.4	102	3	AAW94957
114	73	82.0	14	4	AA90149	Factor VI	187	44	49.4	102	5	AAW85556
115	73	82.0	15	4	AA90148	Factor VI	188	44	49.4	102	6	ABU69528
116	73	82.0	15	8	ADM95580	Tissue fa	189	44	49.4	102	6	ABU66431
117	73	82.0	20	4	AA90144	Factor VI	190	44	49.4	102	7	ADH47337
118	73	82.0	20	4	AA90235	Factor VI	191	44	49.4	102	8	ADJ21256
119	73	82.0	20	4	AA90216	Factor VI	192	44	49.4	116	4	AAW86882
120	73	82.0	20	4	AA90210	Factor VI	193	44	49.4	117	7	ADP58766
121	73	82.0	20	4	AA90211	Factor VI	194	44	49.4	139	8	ADX90050
122	73	82.0	20	4	AA90232	Factor VI	195	44	49.4	216	7	ABO74302
123	73	82.0	20	4	AA90217	Factor VI	196	44	49.4	257	7	ABO83122
124	73	82.0	20	6	ABR82325	Clone AA/	197	44	49.4	257	7	ADW26697
125	73	82.0	20	6	ABR82328	Clone AD	198	44	49.4	350	7	ADW26697
126	73	82.0	20	6	ABR82336	Factor X	199	44	49.4	597	8	ADX93167
127	73	82.0	20	6	ABR82326	Clone AB	200	44	49.4	13	6	ADA03303
128	73	82.0	20	6	ABR82334	Clone AK	201	44	49.4	21	6	ADA03322
129	73	82.0	20	6	ABR82334	Factor VI	202	44	49.4	21	6	ABR56602
130	72	80.9	13	4	AA90228	Factor VI	203	43.5	48.9	59	4	AAW88821
131	72	80.9	13	4	AA90228	Factor VI	204	43.5	48.9	87	4	AAU65802
132	72	80.9	18	4	AA90223	Factor VI	205	43.5	48.9	87	4	AAU62091
133	72	80.9	20	4	AA90213	Factor VI	206	43.5	48.9	87	6	ABM56610
134	72	80.9	20	4	AA90234	Factor VI	207	43.5	48.9	87	6	ABM56321
135	72	80.9	20	4	AA90143	Factor VI	208	43.5	48.9	118	8	ABU99121
136	72	80.9	20	4	AA90239	Factor VI	209	43.5	48.9	118	8	ABU99121
137	72	80.9	20	6	ABR82340	Clone AG	210	43.5	48.9	118	8	ADW93807
138	72	80.9	20	6	ABR82349	Factor X	211	43.5	48.9	214	7	ADJ11392
139	72	80.9	20	6	ABR82324	Clone A-5	212	43.5	48.9	214	7	ADJ11738
140	71	79.8	13	4	AA90164	Factor VI	213	43.5	48.9	239	6	ABU22255
141	71	79.8	15	8	ADM96609	Tissue fa	214	43.5	48.9	239	8	AD126444
142	71	79.8	20	4	AA90208	Factor VI	215	43.5	48.9	239	8	AD126437
143	71	79.8	20	6	ABR82335	Clone AL	216	43.5	48.9	299	9	AD126437
144	71	79.8	24	4	AA90198	Factor VI	217	43	48.3	15	9	AEA09098
145	70	78.7	20	4	AA90230	Factor VI	218	43	48.3	15	9	AEA09245
146	69	77.5	10	6	ABR82345	Factor X	219	43	48.3	66	4	ABR37912
147	68	76.4	20	4	AA90238	Factor VI	220	43	48.3	66	4	AAW31322
148	67	75.3	15	8	ADM96614	Tissue fa	221	43	48.3	66	4	AAW71045
149	67	75.3	20	4	AA90233	Factor VI	222	43	48.3	66	4	AAW58544
150	67	75.3	22	4	AA90203	Factor VI	223	43	48.3	66	4	ABG52760
151	65	73.0	9	4	AA90157	Factor VI	224	43	48.3	66	5	ABG40838
152	65	73.0	13	4	AA90162	Factor VI	225	43	48.3	227	7	ABO81633
153	65	73.0	13	4	AA90225	Factor VI	226	43	48.3	361	4	AAW79698
154	65	73.0	13	6	ABR82346	Factor X	227	43	48.3	361	4	AAW90400
155	62	69.7	11	4	AA90152	Factor VI	228	43	48.3	361	5	ABW07663
156	62	69.7	13	4	AA90166	Factor VI	229	43	48.3	361	5	AAW51076
157	61	68.5	16	4	AA90163	Factor VI	230	43	48.3	458	2	AAW63704
158	60	67.4	8	4	AA90158	Factor VI	231	43	48.3	521	8	ADN10631
159	59	66.3	9	4	AA90155	Factor VI	232	43	48.3	521	8	ADN10679
160	57	64.0	10	4	AA90153	Factor VI	233	43	48.3	521	9	ADZ65319
161	54	60.7	8	4	AA90156	Factor VI	234	43	48.3	521	9	ADZ65367
162	50	56.2	8	4	ADG23484	Bacterial	235	43	48.3	521	9	ADZ65914
163	49	55.1	8	4	AA90154	Factor VI	236	43	48.3	521	9	ADZ65866
164	49	55.1	141	3	AA90154	Factor VI	237	43	48.3	521	7	ADZ65866
165	49	55.1	196	3	AA90154	Factor VI	238	43	48.3	521	7	ADZ65866
166	49	55.1	230	3	AA90154	Factor VI	239	43	48.3	521	7	ADZ65866
167	49	55.1	230	3	AA90154	Factor VI	240	43	48.3	521	7	ADZ65866
168	49	55.1	533	3	AA90154	Factor VI	241	43	48.3	521	7	ADZ65866
169	47	52.8	27	9	ADV76482	Human HER	242	42	47.2	13	6	ADA03305
170	47	52.8	27	9	ADV76463	Human HER	243	42	47.2	13	6	ABR56675

AA90320	Pertussis
ABO81065	Pseudomon
ABG26675	Novel hum
ABW70322	Drosophil
ABO57247	Human gen
ADM05346	Human pro
AAW9397	S. antibio
AAW19888	Peptide #
ABR39831	Peptide #
AAW3424	Peptide #
ABW22435	Protein #
AAW73218	Human bon
AAW60559	Human bra
ABG54934	Human liv
ABG43065	Human pep
ABO60599	Human gen
AAW94957	Human sec
AAW85556	Clone #50
ABU69528	Human lum
ABU66431	Lung can
ADH47337	Human lum
ADJ21256	Human lum
AAW86882	Human imm
ADP58766	Human pol
ADX90050	Plant ful
ABO74302	Pseudomon
ABO83122	Pseudomon
ADW26697	Hypertet
ADX93167	Plant ful
ADA03303	Angiotens
ABR56673	Angiotens
ADA03232	Angiotens
ABR56602	Angiotens
AAW88821	Human imm
AAU65802	Propionib
AAU62091	Propionib
ABM56610	Propionib
ABM56321	Novel hum
ABU99121	Novel hum
ABU93807	Human NOV
ADJ11392	Rice prot
ADJ11738	Rice prot
ABU22255	Protein e
AD126444	B. pseudo
AD126437	B. majlei
AAZ02028	Novel hum
AAO9098	Bacterial
AAO9245	Bacterial
ABD37912	Peptide #
AAW31322	Peptide #
AAW71045	Human bon
AAW58544	Human bra
ABG52760	Human liv
ABG40838	Human pep
ABO81633	Pseudomon
AAW79698	Cornebacc
AAW90400	C. glutami
ABW07663	C. glutami
AAW51076	Cornebacc
AAW63704	Rat IRS1
ADN10631	Nicotiana
ADN10679	Nicotiana
ADZ65319	Tobacco c
ADZ65367	Tobacco c
ADZ65914	Tobacco c
ADZ65866	Tobacco c
ADZ65866	Rat Prote
ABM90150	Rice abio
AAW72894	Human met
ABU20216	Protein e
AAW30813	Amilo aci
ADA03305	Angiotens
ABR56675	Angiotens

315	41	46.1
316	41	46.1

390	40	44.9	153	4	AAU20019	Aau20019 Human liv	463	40	44.9	1080	9	ADY19552	Ady19552 PRO polyp
391	40	44.9	153	5	ABP40880	Abp40880 Human liv	464	40	44.9	1515	9	ABE96740	Abep96740 Human EGF
392	40	44.9	153	7	ADJ14998	Adj14998 Human liv	465	39.5	44.4	18	2	AAW67536	Igf-1/IGF
393	40	44.9	154	8	ADP07805	Adp07805 Human sec	466	39.5	44.4	18	4	AAG63773	ABG63773 Synthetic
394	40	44.9	154	8	ADP07765	Adp07765 Human sec	467	39.5	44.4	18	5	ABBS7695	IGFBP-3 b
395	40	44.9	164	5	ABG64899	Abg64899 Human alb	468	39.5	44.4	18	7	ADH48169	IGFBP-3 b
396	40	44.9	164	5	ABG77036	Abg77036 Human pro	469	39.5	44.4	18	7	ADH48169	IGFBP-3 b
397	40	44.9	164	6	ADA41484	Ada41484 Human sec	470	39.5	44.4	18	8	ADF47660	Insulin-1
398	40	44.9	164	6	ADB08794	Adb08794 Human sec	471	39.5	44.4	18	8	ADG39606	IGFBP-3 b
399	40	44.9	164	7	ADC74598	Adc74598 Human sec	472	39.5	44.4	18	8	ADI62089	IGFBP-3 b
400	40	44.9	164	8	ADL78166	Adl78166 Human f	473	39.5	44.4	18	8	ADI57600	Inhibitor
401	40	44.9	186	5	ABG64900	Abg64900 Human alb	474	39.5	44.4	18	8	ADI57493	Inhibitor
402	40	44.9	186	5	ABG77012	Abg77012 Human pro	475	39.5	44.4	18	8	ADJ56649	Inhibitor
403	40	44.9	186	6	ADA41164	Ada41164 Human sec	476	39.5	44.4	18	8	ADJ58171	Inhibitor
404	40	44.9	186	7	ADC74368	Adc74368 Human sec	477	39.5	44.4	18	8	ADJ45171	Inhibitor
405	40	44.9	186	8	ADG22391	Adg22391 Cyanophag	478	39.5	44.4	18	8	ADM76517	IGFBP-3 b
406	40	44.9	186	8	ADL78167	Adl78167 Human f	479	39.5	44.4	18	8	ADL08285	Inhibitor
407	40	44.9	202	8	ABO60070	AbO60070 Human gen	480	39.5	44.4	18	8	ADN32768	Insulin-1
408	40	44.9	214	8	ABO60070	AbO60070 Human tra	481	39.5	44.4	104	6	ABP68433	Human col
409	40	44.9	217	7	ADC78237	Adc78237 Human sec	482	39.5	44.4	115	4	AAW44359	Murine ES
410	40	44.9	217	8	ADP07760	Adp07760 Human sec	483	39.5	44.4	196	7	ABO74911	Pseudomon
411	40	44.9	228	6	ADB08796	Adb08796 Alloiococ	484	39.5	44.4	262	5	ABG72568	Human hom
412	40	44.9	246	8	ADP99164	Adp99164 Human tra	485	39.5	44.4	422	4	ABG21846	Novel hum
413	40	44.9	280	4	ADG81165	Adg81165 Mycobacte	486	39.5	44.4	444	4	AAG70885	C albican
414	40	44.9	284	4	ABU53092	Abu53092 Human tra	487	39.5	44.4	547	5	ABP73747	Candida a
415	40	44.9	305	5	AAE21282	Aae21282 Mouse Mrg	488	39.5	44.4	554	7	ABO79486	Pseudomon
416	40	44.9	305	8	ADH08508	Adh08508 MrGA2. 3/	489	39	43.8	7	ADP06046	Cell adhe	
417	40	44.9	305	8	ADH08508	Adh08508 MrGA2. 3/	490	39	43.8	10	2	AAAS0903	Cyclic pe
418	40	44.9	331	4	AAG64398	Aag64398 Murine G-p	491	39	43.8	13	6	ADA03314	Angiotens
419	40	44.9	331	5	ABB08769	Abb08769 Mouse G-p	492	39	43.8	13	6	ABR56684	Angiotens
420	40	44.9	374	4	AAU16315	Aau16315 Human nov	493	39	43.8	23	4	ABG64437	Human sec
421	40	44.9	374	6	ABU55384	Abu55384 Human nov	494	39	43.8	30	8	ADS33512	CMET-RGF
422	40	44.9	409	7	ABO71490	AbO71490 Pseudomon	495	39	43.8	31	5	ABR60450	Selective
423	40	44.9	423	8	ADR86088	Adr86088 Aspergill	496	39	43.8	37	6	ABP99775	Human sec
424	40	44.9	435	2	AAW27441	Aaw27441 Oil seed	497	39	43.8	37	6	ABR01268	Human gen
425	40	44.9	443	2	AAW27441	Aaw27441 Oil seed	498	39	43.8	37	6	ABR01268	Human gen
426	40	44.9	450	9	ADY60929	Ady60929 Abiotic s	499	39	43.8	37	6	ADA98353	Human sec
427	40	44.9	539	5	AAW47457	Aaw47457 Human IL-	500	39	43.8	38	3	ABR29821	Human sec
428	40	44.9	564	7	ADC08048	Adc08048 Rice prot	501	39	43.8	59	4	ABBI6550	Human ner
429	40	44.9	866	2	AAW04185	Aaw04185 Human int	502	39	43.8	64	6	ADA23107	Tulipa ge
430	40	44.9	866	2	AAW61272	Aaw61272 Human int	503	39	43.8	66	4	AAU55633	Propionib
431	40	44.9	866	2	AAW92409	Aaw92409 Human IL-	504	39	43.8	66	6	ABM52152	Propionib
432	40	44.9	866	3	AAW97131	Aaw97131 Human int	505	39	43.8	98	4	AAU10578	Human pol
433	40	44.9	866	3	AAW97181	Aaw97181 Human int	506	39	43.8	104	4	AAU28218	Novel hum
434	40	44.9	866	3	AAW03807	Aaw03807 Human int	507	39	43.8	117	4	AAU19353	Peptide #
435	40	44.9	866	3	AAW99941	Aaw99941 Human IL-	508	39	43.8	117	4	ABR38710	Peptide #
436	40	44.9	866	4	ABG62066	Abg62066 Human IL-	509	39	43.8	117	4	ABM32176	Peptide #
437	40	44.9	866	4	AAW72754	Aaw72754 Human int	510	39	43.8	117	4	ABM32176	Peptide #
438	40	44.9	866	5	ABW78079	Abw78079 Amino aci	511	39	43.8	117	4	AAW71896	Protein #
439	40	44.9	866	7	ADD25546	Ad25546 Bifidobacte	512	39	43.8	117	4	AAW59343	Human bon
440	40	44.9	866	8	ADJ88265	Adj88265 Human IL-	513	39	43.8	117	4	ABG53578	Human bra
441	40	44.9	866	8	ADL24269	Adl24269 Human IL-	514	39	43.8	117	5	ABG41709	Human liv
442	40	44.9	866	8	ADP09702	Adp09702 Human IL-	515	39	43.8	126	4	ABG07221	Novel hum
443	40	44.9	866	8	ADQ1252	Adq1252 Human int	516	39	43.8	135	3	AAW41247	Novel hum
444	40	44.9	866	8	ADQ1308	Adq1308 Human int	517	39	43.8	135	7	ABO75955	Pseudomon
445	40	44.9	866	9	ADY19986	Ady19986 PRO polyp	518	39	43.8	165	4	ABG02068	Novel hum
446	40	44.9	866	9	ADY15612	Ady15612 PRO polyp	519	39	43.8	172	7	ADM06019	Human pro
447	40	44.9	898	8	ADH61286	Adh61286 INTSIG pr	520	39	43.8	189	8	ADR10104	Human pro
448	40	44.9	900	2	AAW96264	Aaw96264 Human axi	521	39	43.8	189	8	ADR10053	Human pro
449	40	44.9	900	4	AAG68175	Aag68175 Wnt signa	522	39	43.8	229	3	ABG29737	Arabidops
450	40	44.9	900	6	ABR41099	AbR41099 Human Wnt	523	39	43.8	251	6	ABU18601	Protein e
451	40	44.9	900	7	ADB98719	Adb98719 Human axi	524	39	43.8	261	7	ADM04828	Human gen
452	40	44.9	900	7	ADD14026	Add14026 Human src	525	39	43.8	267	8	ABO60229	Human pro
453	40	44.9	900	7	ADG82515	Adg82515 Human pro	526	39	43.8	268	7	ADJ68544	Human hea
454	40	44.9	912	5	ABU65175	Abu65175 Human NOV	527	39	43.8	269	2	AAW35965	Extended
455	40	44.9	912	8	ADH62001	Adh62001 Human nov	528	39	43.8	269	8	ADP19273	Human sec
456	40	44.9	958	8	ADH61287	Adh61287 INTSIG pr	529	39	43.8	270	8	ADU00115	Amino aci
457	40	44.9	1080	5	AAE25346	Aae25346 Human ade	530	39	43.8	273	3	AAW47105	Arabidops
458	40	44.9	1080	6	AAE37343	Aae37343 Human 980	531	39	43.8	273	3	AAW23339	Arabidops
459	40	44.9	1080	8	ADQ89872	Adq89872 Antagonis	532	39	43.8	287	3	AAW23338	Arabidops
460	40	44.9	1080	8	ADQ98818	Adq98818 Antagonis	533	39	43.8	287	3	AAW47104	Arabidops
461	40	44.9	1080	8	ADU06598	Adu06598 Novel bro	534	39	43.8	296	6	ADA36195	Acinetoba
462	40	44.9	1080	9	ADY15172	Ady15172 PRO polyp	535	39	43.8	303	8	ADN00724	Human SLT

536	39	43.8	308	2	AAV14071	Mitogenic	609	39	43.8	459	4	AAAB82973	Human G p
537	39	43.8	308	3	AGC23337	Arabidops	610	39	43.8	459	5	ABP43596	FLJ10904
538	39	43.8	308	3	AGC47103	Arabidops	611	39	43.8	472	8	ADS44374	Bacterial
539	39	43.8	311	7	ABO66496	Klebsiell	612	39	43.8	474	7	ABD74569	Mycobacte
540	39	43.8	319	6	ABU18300	Protein e	613	39	43.8	479	8	ADR86206	Aspergill
541	39	43.8	323	7	ABO74001	Pseudomon	614	39	43.8	483	4	ADM20125	Protein e
542	39	43.8	323	6	ABE31489	Dog MCH-2	615	39	43.8	485	7	ADF04332	Bacterial
543	39	43.8	330	7	ABW01469	Canine MC	616	39	43.8	504	8	ABO79496	Pseudomon
544	39	43.8	330	7	AD224756	Cynomelgu	617	39	43.8	548	8	ADY22396	Plant ful
545	39	43.8	330	7	ADG98837	Cynomelgu	618	39	43.8	559	8	ADQ66215	Novel hum
546	39	43.8	330	7	ADG98827	Canine me	619	39	43.8	595	4	AAU23294	Novel cen
547	39	43.8	330	7	ADG98838	Cynomelgu	620	39	43.8	595	4	AAU87547	Novel hum
548	39	43.8	330	7	ADH53361	Canine MC	621	39	43.8	595	8	ADI54862	Novel hum
549	39	43.8	335	5	AAE18650	Human G-p	622	39	43.8	868	4	ABG20571	Novel hum
550	39	43.8	335	3	AGC29736	Arabidops	623	39	43.8	874	4	ABG26108	Novel hum
551	39	43.8	340	3	AAE23540	Human G-p	624	39	43.8	997	4	ABG15941	Novel hum
552	39	43.8	340	3	AAU25610	Human G-p	625	39	43.8	1024	5	ABB04860	LDL recep
553	39	43.8	340	4	AAE68428	Amino aci	626	39	43.8	1078	4	ABB61252	Drosophill
554	39	43.8	340	4	AAE51567	Human mel	627	39	43.8	1162	4	ABG05052	Novel hum
555	39	43.8	340	4	AAE51568	Human mel	628	39	43.8	1253	4	AAAM39117	Human pol
556	39	43.8	340	4	AAE68893	Human AXO	629	39	43.8	1253	4	AAAM39117	Human pol
557	39	43.8	340	4	AAU04381	Human G-p	630	39	43.8	1253	7	ABD79866	Mouse put
558	39	43.8	340	5	AAU77532	G protein	631	39	43.8	1255	8	ADQ66660	Novel hum
559	39	43.8	340	5	ABU07986	Human sev	632	39	43.8	1281	8	ADP55147	Human PRO
560	39	43.8	340	5	AAU97733	Human TGR	633	39	43.8	1281	8	ADP24771	PRO polytp
561	39	43.8	340	6	AAE31490	Ferret MC	634	39	43.8	1335	4	AAAM40903	Human ORF
562	39	43.8	340	6	AAE31492	Human MCH	635	39	43.8	1335	3	AAAB40324	Human ORF
563	39	43.8	340	6	AAE31491	Rhesus mo	636	39	43.8	1393	3	AAAB40324	Human ORF
564	39	43.8	340	6	ABP81746	Human mel	637	39	43.8	1393	3	AAAB40324	Human ORF
565	39	43.8	340	6	ABP81746	Human mel	638	39	43.8	1393	3	AAAB40324	Human ORF
566	39	43.8	340	6	AAE35562	Human mel	639	39	43.8	1393	3	AAAB40324	Human ORF
567	39	43.8	340	6	AAO27467	Human mel	640	39	43.8	1393	3	AAAB40324	Human ORF
568	39	43.8	340	7	ABW00463	Human G p	641	39	43.8	1393	3	AAAB40324	Human ORF
569	39	43.8	340	7	ABW01467	Monkey MC	642	39	43.8	1393	3	AAAB40324	Human ORF
570	39	43.8	340	7	ABW01468	Monkey MC	643	39	43.8	1393	3	AAAB40324	Human ORF
571	39	43.8	340	7	ABW01468	Monkey MC	644	39	43.8	1393	3	AAAB40324	Human ORF
572	39	43.8	340	7	AD224736	Monkey me	645	39	43.8	1393	3	AAAB40324	Human ORF
573	39	43.8	340	7	ADG98824	Cynomelgu	646	39	43.8	1393	3	AAAB40324	Human ORF
574	39	43.8	340	7	ADG98849	Human MCH	647	39	43.8	1393	3	AAAB40324	Human ORF
575	39	43.8	340	7	ADG98846	Cynomelgu	648	39	43.8	1393	3	AAAB40324	Human ORF
576	39	43.8	340	7	ADG98846	Cynomelgu	649	39	43.8	1393	3	AAAB40324	Human ORF
577	39	43.8	340	7	ADG98846	Cynomelgu	650	39	43.8	1393	3	AAAB40324	Human ORF
578	39	43.8	340	7	ADG98846	Cynomelgu	651	39	43.8	1393	3	AAAB40324	Human ORF
579	39	43.8	340	7	ADG98846	Cynomelgu	652	39	43.8	1393	3	AAAB40324	Human ORF
580	39	43.8	340	7	ADH53356	Cynomelgu	653	39	43.8	1393	3	AAAB40324	Human ORF
581	39	43.8	340	7	ADH53358	Cynomelgu	654	39	43.8	1393	3	AAAB40324	Human ORF
582	39	43.8	340	8	ADN00702	Human SLT	655	39	43.8	1393	3	AAAB40324	Human ORF
583	39	43.8	340	8	ADN00702	Human GPC	656	39	43.8	1393	3	AAAB40324	Human ORF
584	39	43.8	340	8	ADN15185	Human G p	657	39	43.8	1393	3	AAAB40324	Human ORF
585	39	43.8	340	8	ADN15185	Human G p	658	39	43.8	1393	3	AAAB40324	Human ORF
586	39	43.8	340	9	ADW44659	Human RUP	659	39	43.8	1393	3	AAAB40324	Human ORF
587	39	43.8	340	9	ADY57308	Human RUP	660	39	43.8	1393	3	AAAB40324	Human ORF
588	39	43.8	341	6	ADA34837	Acinetoba	661	39	43.8	1393	3	AAAB40324	Human ORF
589	39	43.8	346	7	ADG98853	Cynomelgu	662	39	43.8	1393	3	AAAB40324	Human ORF
590	39	43.8	346	7	ADG98843	Cynomelgu	663	39	43.8	1393	3	AAAB40324	Human ORF
591	39	43.8	346	7	ADG98843	Cynomelgu	664	39	43.8	1393	3	AAAB40324	Human ORF
592	39	43.8	348	7	ADG98835	Cynomelgu	665	39	43.8	1393	3	AAAB40324	Human ORF
593	39	43.8	348	7	ADG98835	Cynomelgu	666	39	43.8	1393	3	AAAB40324	Human ORF
594	39	43.8	359	7	ABW01474	Monkey MC	667	39	43.8	1393	3	AAAB40324	Human ORF
595	39	43.8	359	7	ADH53372	Cynomelgu	668	39	43.8	1393	3	AAAB40324	Human ORF
596	39	43.8	361	7	ADP06422	Bacterial	669	39	43.8	1393	3	AAAB40324	Human ORF
597	39	43.8	370	7	ADG98839	Cynomelgu	670	39	43.8	1393	3	AAAB40324	Human ORF
598	39	43.8	382	4	ABG21902	Novel hum	671	39	43.8	1393	3	AAAB40324	Human ORF
599	39	43.8	382	4	ADN19881	Protein e	672	39	43.8	1393	3	AAAB40324	Human ORF
600	39	43.8	385	4	ADG98840	Cynomelgu	673	39	43.8	1393	3	AAAB40324	Human ORF
601	39	43.8	398	4	ABG28865	Novel hum	674	39	43.8	1393	3	AAAB40324	Human ORF
602	39	43.8	417	7	ABO79667	Pseudomon	675	39	43.8	1393	3	AAAB40324	Human ORF
603	39	43.8	428	3	AAE29735	Arabidops	676	39	43.8	1393	3	AAAB40324	Human ORF
604	39	43.8	429	7	ADB74319	Mycobacte	677	39	43.8	1393	3	AAAB40324	Human ORF
605	39	43.8	446	5	ABE89270	Human pol	678	39	43.8	1393	3	AAAB40324	Human ORF
606	39	43.8	459	4	AAE93830	Human pro	679	39	43.8	1393	3	AAAB40324	Human ORF
607	39	43.8	459	4	AAE93831	Human pro	680	39	43.8	1393	3	AAAB40324	Human ORF
608	39	43.8	459	4	AAE94812	Human pro	681	39	43.8	1393	3	AAAB40324	Human ORF

682	38	42.7	34	4	AAM63567	Aam63567 Human bra	755	38	42.7	207	3	AAG29277	Arabidops
683	38	42.7	34	4	ASG58088	Human liv	756	38	42.7	212	3	AAV50922	Human fet
684	38	42.7	34	5	ASG58088	Human pep	757	38	42.7	212	5	ABB05669	Human tra
685	38	42.7	48	7	ADB49266	WW domain	758	38	42.7	212	5	ABB04323	Human vac
686	38	42.7	49	4	AAM13924	Peptide #	759	38	42.7	213	4	AAU31274	Novel hum
687	38	42.7	49	4	ABB32869	Peptide #	760	38	42.7	214	1	AAAP81784	Sequence
688	38	42.7	49	4	AAM26330	Peptide #	761	38	42.7	214	2	AAAR22367	SI Vmac239
689	38	42.7	49	4	ABB27698	Human pep	762	38	42.7	214	2	AAW89315	SI Vmac239
690	38	42.7	49	4	ABB18351	Protein #	763	38	42.7	214	7	ADB66954	E. coli K
691	38	42.7	49	4	AAM66055	Human bon	764	38	42.7	214	9	ADY73675	Escherich
692	38	42.7	49	4	AAM53671	Human bra	765	38	42.7	214	9	AEA28098	HIV-1 vir
693	38	42.7	49	4	ABG47721	Human liv	766	38	42.7	215	1	AAAP80812	Sequence
694	38	42.7	49	4	ABM01667	Peptide #	767	38	42.7	215	1	AAAP81774	Sequence
695	38	42.7	49	5	ABG35703	Human pep	768	38	42.7	215	1	AAAP80811	Sequence
696	38	42.7	49	8	ABO56370	Human gen	769	38	42.7	215	2	AAAR04026	Q gene pr
697	38	42.7	53	4	AAU31425	Novel hum	770	38	42.7	215	2	AAAR20600	ROD HIV-2
698	38	42.7	55	4	AAU63516	Propionib	771	38	42.7	215	2	AAAW13058	HIV-2 pro
699	38	42.7	55	6	ABM60035	Propionib	772	38	42.7	215	3	AAAY51979	HIV-2 ROD
700	38	42.7	60	4	ABG09886	Novel hum	773	38	42.7	215	6	ADA07962	HIV-2 Q p
701	38	42.7	65	4	AAU50938	Propionib	774	38	42.7	215	7	ADD30184	Plant yie
702	38	42.7	65	6	ABM47457	Propionib	775	38	42.7	215	8	ADI43991	Plant tra
703	38	42.7	69	8	ADU20698	Human sec	776	38	42.7	215	8	ADL23700	HIV-2 ROD
704	38	42.7	70	7	ADU13869	Human end	777	38	42.7	216	9	AEA28100	HIV-1 vir
705	38	42.7	73	4	AAU55989	Propionib	778	38	42.7	216	9	AEA28099	HIV-1 vir
706	38	42.7	73	6	ABM52508	Propionib	779	38	42.7	228	7	ADB64675	Human pro
707	38	42.7	74	8	ADP29545	Human sec	780	38	42.7	240	8	ADJ79495	Epstein-B
708	38	42.7	76	4	ABG06758	Novel hum	781	38	42.7	241	6	ABU19956	Protein e
709	38	42.7	76	4	AAU31424	Novel hum	782	38	42.7	246	8	ADJ79590	Human imm
710	38	42.7	79	4	AAU73536	Human col	783	38	42.7	261	2	AAAY43961	Drosophil
711	38	42.7	81	4	AAU00286	Immunogen	784	38	42.7	262	2	AAW27262	Plant ste
712	38	42.7	90	2	AAU12173	Human 5'	785	38	42.7	262	3	AAG29276	Arabidops
713	38	42.7	90	4	ABG17940	Novel hum	786	38	42.7	262	6	ABP71247	A. thalia
714	38	42.7	90	6	ABO00927	Polypepti	787	38	42.7	262	8	ADT55702	Plant pol
715	38	42.7	90	6	ADF60411	Human con	788	38	42.7	262	8	ADP90941	Ovine pro
716	38	42.7	90	8	ADK70974	Corn GL5	789	38	42.7	279	8	ADC64234	Human sma
717	38	42.7	92	8	ADK95453	Plant ful	790	38	42.7	283	7	ADC64234	T cell ac
718	38	42.7	95	8	ADK70972	Corn GL4	791	38	42.7	284	8	ADQ95982	Arabidops
719	38	42.7	97	4	AAM84451	Human imm	792	38	42.7	293	3	AAG08725	Arabidops
720	38	42.7	97	4	AAU58891	Propionib	793	38	42.7	297	7	ABO80096	Pseudomon
721	38	42.7	97	6	ABM55410	Propionib	794	38	42.7	302	3	ABG08724	Arabidops
722	38	42.7	100	6	ADAL4351	Mouse spe	795	38	42.7	302	3	ADT56473	Plant pol
723	38	42.7	102	8	ADK75809	Plant ful	796	38	42.7	304	8	ADN10701	Nicotiana
724	38	42.7	116	4	AAU53148	Propionib	797	38	42.7	304	9	ADZ65389	Tobacco c
725	38	42.7	116	6	ABM49667	Propionib	798	38	42.7	304	9	ADZ65936	Tobacco c
726	38	42.7	118	3	AG040474	Human sec	799	38	42.7	314	5	ABP41487	Human ova
727	38	42.7	123	5	AAAM48387	Human YSK	800	38	42.7	323	2	AAW14799	Type 5 17
728	38	42.7	125	3	AAAG26755	Zea may	801	38	42.7	323	4	AAW78471	Human pro
729	38	42.7	127	8	ADK71162	Plant ful	802	38	42.7	323	6	ABR47388	Breast ca
730	38	42.7	135	4	ABG27560	Novel hum	803	38	42.7	323	6	ABU89739	Protein d
731	38	42.7	136	4	ABG12755	Novel hum	804	38	42.7	323	6	AAE37820	Bovine pr
732	38	42.7	136	4	ADM05066	Human pro	805	38	42.7	323	6	AAE37819	Bovine pr
733	38	42.7	140	3	AAV56712	Amino aci	806	38	42.7	323	6	AAE37814	Human ald
734	38	42.7	146	7	ABO68560	Pseudomon	807	38	42.7	323	7	ADZ656524	Human ald
735	38	42.7	152	4	AAAB76871	Human lun	808	38	42.7	323	7	ADD48658	Human pro
736	38	42.7	152	4	AAAB76867	Human lun	809	38	42.7	323	7	ADD48658	Human pro
737	38	42.7	152	5	AAU85526	L840P lun	810	38	42.7	323	8	ADJ75576	Marker ge
738	38	42.7	152	5	AAU85522	L840P lun	811	38	42.7	323	8	ADL61228	Human ald
739	38	42.7	152	6	ABU69498	Human lun	812	38	42.7	323	8	ADN04390	Antipsori
740	38	42.7	152	6	ABU69494	Human lun	813	38	42.7	323	8	ADN04390	Antipsori
741	38	42.7	152	6	ABU66400	Lung canc	814	38	42.7	323	8	ADQ18101	Protein #
742	38	42.7	152	6	ABU66396	Lung canc	815	38	42.7	323	8	ADQ18101	Human sof
743	38	42.7	152	7	ADH46314	Human lun	816	38	42.7	323	8	ADP90940	Bovine lu
744	38	42.7	152	7	ADH46306	Human lun	817	38	42.7	323	8	ADP90940	Bovine lu
745	38	42.7	152	8	ADJ20225	Human lun	818	38	42.7	323	8	ADP90940	Bovine li
746	38	42.7	152	8	ADJ20233	Human lun	819	38	42.7	323	8	ADP90940	Bovine ch
747	38	42.7	155	3	AAAB53583	Human col	820	38	42.7	323	8	ADP90943	Novel bro
748	38	42.7	155	5	ABU10596	cDNA enco	821	38	42.7	323	8	ADU06724	Novel bro
749	38	42.7	162	3	ABAB42813	Human ORF	822	38	42.7	325	4	AAW79455	Human pro
750	38	42.7	162	7	ABO70510	Pseudomon	823	38	42.7	325	6	AAW79455	Human pro
751	38	42.7	165	5	ABG34854	Human cin	824	38	42.7	330	6	ABP70817	Human C1Q
752	38	42.7	173	4	AAU32398	Novel hum	825	38	42.7	330	6	ABU99123	Novel hum
753	38	42.7	182	7	ABO78099	Pseudomon	826	38	42.7	331	4	ADM93811	Human NOV
754	38	42.7	187	3	AAAB25413	Pinus rad	827	38	42.7	364	7	ADM05927	Human dia

828	38	42.7	374	7	ABO70729	Pseudomon
829	38	42.7	386	3	AB25527	Pinus rad
830	38	42.7	388	4	AB58256	Drosophil
831	38	42.7	404	9	AEA43200	Pethydril
832	38	42.7	406	8	ADH22267	ORF2 prot
833	38	42.7	445	7	ABO76084	Pseudomon
834	38	42.7	453	7	AB50206	Human tra
835	38	42.7	456	5	ABP69604	Human pol
836	38	42.7	456	6	ADA54532	Human pro
837	38	42.7	470	8	ADN20610	Bacterial
838	38	42.7	480	5	ABU05987	M. tuberc
839	38	42.7	481	2	AA72095	Human mgl
840	38	42.7	481	4	AB52992	Escherich
841	38	42.7	498	4	ABG09680	Novel hum
842	38	42.7	518	8	ADN10713	Nicotiana
843	38	42.7	518	9	ADZ65399	Tobacco c
844	38	42.7	518	9	ADZ65948	Tobacco c
845	38	42.7	531	5	ABP65909	Bifidobac
846	38	42.7	545	4	ABB62920	Drosophil
847	38	42.7	601	6	ABJ25612	Aspergill
848	38	42.7	608	7	ADL22693	Human dis
849	38	42.7	632	8	ADR08956	Human pro
850	38	42.7	660	3	AA74600	Neisseria
851	38	42.7	660	3	AA74601	Neisseria
852	38	42.7	660	3	AA74602	Neisseria
853	38	42.7	675	5	AAU91074	Neisseria
854	38	42.7	675	6	ABP78636	N. gonorr
855	38	42.7	738	2	AA701070	Human l(3
856	38	42.7	772	2	AA701069	Human l(3
857	38	42.7	782	8	AD518117	73-845 of
858	38	42.7	782	9	AEA94882	Human his
859	38	42.7	782	9	AB56253	Histone d
860	38	42.7	783	8	ADN27164	Bacterial
861	38	42.7	817	4	AA956640	Human pro
862	38	42.7	851	3	AA796165	Schizosac
863	38	42.7	851	3	ADN19660	Bacterial
864	38	42.7	867	2	AA72093	Human mgl
865	38	42.7	876	7	ADN04296	Human pro
866	38	42.7	881	9	AEA28469	Arabidops
867	38	42.7	898	9	ADZ67613	Chimeric
868	38	42.7	907	9	ADZ67611	Chimeric
869	38	42.7	910	9	ADZ67609	Chimeric
870	38	42.7	912	9	ADZ67607	Chimeric
871	38	42.7	915	2	AA72097	Human mgl
872	38	42.7	915	2	AA72097	Human mgl
873	38	42.7	915	5	ABG95165	Human GPC
874	38	42.7	915	5	ABG95155	Human GPC
875	38	42.7	915	5	ABG95164	Human GPC
876	38	42.7	915	5	ABG95166	Human GPC
877	38	42.7	915	5	ABG95163	Human GPC
878	38	42.7	915	6	AAE30199	Rat metab
879	38	42.7	915	6	ABP81849	Human met
880	38	42.7	915	7	ADD48384	Rat Prote
881	38	42.7	915	7	ABE55969	Human Pro
882	38	42.7	915	7	ABE55967	Rat Prote
883	38	42.7	915	7	ADJ93191	Human met
884	38	42.7	915	8	ADO29103	Human nov
885	38	42.7	915	8	ADO29104	Mouset nov
886	38	42.7	915	9	ADZ67603	Human met
887	38	42.7	915	9	ABE87480	Human met
888	38	42.7	922	2	AA72098	Human mgl
889	38	42.7	1052	4	ABE71502	Drosophil
890	38	42.7	1215	5	AAE22856	Human his
891	38	42.7	1215	5	AAU99661	Human his
892	38	42.7	1215	7	ADZ67603	Human his
893	38	42.7	1215	8	ADH35172	Human HDA
894	38	42.7	1215	8	ADH43340	Human cla
895	38	42.7	1215	9	ADW12277	Human his
896	38	42.7	1280	8	ABM85134	Human dia
897	38	42.7	1280	8	ABM85135	Human dia
898	38	42.7	1280	8	ABM85136	Human dia
899	38	42.7	1280	8	ABM85133	Human dia
900	38	42.7	1280	8	ABM85132	Human dia

901	38	42.7	1394	4	AA20497	Maize P-g
902	38	42.7	1402	4	AAE02402	Sorghum d
903	38	42.7	1504	4	AB60358	Drosophil
904	38	42.7	1620	8	ADQ93770	Antagonis
905	38	42.7	3077	1	AAQ93283	Sequence
906	38	42.7	3211	1	ADP81769	Rice prot
907	38	42.7	3972	1	ADC08191	Angiotens
908	37.5	42.1	13	6	ADA03320	Angiotens
909	37.5	42.1	13	6	AB56690	Angiotens
910	37.5	42.1	94	4	AA57651	KIAA0561
911	37.5	42.1	94	4	AA58061	PDZ encod
912	37.5	42.1	94	4	AA55860	PDZ domai
913	37.5	42.1	94	5	ABJ05326	Human imm
914	37.5	42.1	97	4	AA91013	Human pro
915	37.5	42.1	117	6	AD55314	Human pro
916	37.5	42.1	117	8	ADM87374	Human pro
917	37.5	42.1	226	3	AA34827	Gene 17 h
918	37.5	42.1	243	4	ABG17504	Novel hum
919	37.5	42.1	265	6	ABR43217	Human IRA
920	37.5	42.1	308	6	ABR43223	Human asp
921	37.5	42.1	743	8	ADU24126	Human dia
922	37.5	42.1	915	8	ABM84530	Human dia
923	37.5	42.1	917	8	ABM84529	Human dia
924	37.5	42.1	1076	8	ADS24798	Bacterial
925	37	41.6	5	4	AA90242	Factor VI
926	37	41.6	10	2	AA50921	Cyclic pe
927	37	41.6	10	2	AA50899	Cyclic pe
928	37	41.6	16	8	ADS33348	CMET-HGF
929	37	41.6	33	2	AA293328	HDX prote
930	37	41.6	38	4	AA18829	Peptide #
931	37	41.6	38	4	AB37939	Peptide #
932	37	41.6	38	4	AA31349	Peptide #
933	37	41.6	38	4	AB23191	Protein #
934	37	41.6	38	4	AA71072	Human bon
935	37	41.6	38	4	AA58571	Human bra
936	37	41.6	38	4	ABG52787	Human liv
937	37	41.6	38	5	ABG40865	Human pep
938	37	41.6	44	4	AA85762	Human imm
939	37	41.6	46	3	AA51398	Human sec
940	37	41.6	46	4	AB38221	Peptide #
941	37	41.6	46	4	AA31652	Peptide #
942	37	41.6	46	4	AA23403	Protein #
943	37	41.6	46	4	AA71371	Human bon
944	37	41.6	46	4	AA58854	Human bra
945	37	41.6	46	4	AB53076	Human liv
946	37	41.6	46	4	ABG41172	Human pep
947	37	41.6	46	5	ABG41172	Polypepti
948	37	41.6	48	7	ADD44528	Propionib
949	37	41.6	50	4	AAU64299	Propionib
950	37	41.6	50	6	ABM60818	Human nov
951	37	41.6	54	4	AAU21563	Human gen
952	37	41.6	55	4	AAE01567	Human alb
953	37	41.6	55	5	ABG63789	Albumin f
954	37	41.6	55	8	ADL77054	Albumin f
955	37	41.6	57	4	AAU48294	Propionib
956	37	41.6	57	6	ABM44813	Propionib
957	37	41.6	65	5	ABG77117	Prostate
958	37	41.6	66	4	AB212407	Human bon
959	37	41.6	68	4	AAU57997	Human imm
960	37	41.6	70	4	AAU57997	Propionib
961	37	41.6	70	6	ABM54516	Rat EST e
962	37	41.6	75	4	AA23864	Human ORF
963	37	41.6	81	4	AA84011	Human imm
964	37	41.6	83	4	AA84003	Human imm
965	37	41.6	85	4	AA84003	Human imm
966	37	41.6	85	8	ADX88001	Plant ful
967	37	41.6	87	8	ABO57036	Lung spec
968	37	41.6	90	8	ADR98938	Human gen
969	37	41.6	98	4	AB70639	Drosophil
970	37	41.6	98	8	ADL04949	M. catar
971	37	41.6	99	4	AA73939	Human col
972	37	41.6	104	4	AA96513	Human rep
973	37	41.6				

901	38	42.7	1394	4	AA20497	Maize P-g
902	38	42.7	1402	4	AAE02402	Sorghum d
903	38	42.7	1504	4	AB60358	Drosophil
904	38	42.7	1620	8	ADQ93770	Antagonis
905	38	42.7	3077	1	AAQ93283	Sequence
906	38	42.7	3211	1	ADP81769	Rice prot
907	38	42.7	3972	1	ADC08191	Angiotens
908	37.5	42.1	13	6	ADA03320	Angiotens
909	37.5	42.1	13	6	AB56690	Angiotens
910	37.5	42.1	94	4	AA57651	KIAA0561
911	37.5	42.1	94	4	AA58061	PDZ encod
912	37.5	42.1	94	4	AA55860	PDZ domai
913	37.5	42.1	94	5	ABJ05326	Human imm
914	37.5	42.1	97	4	AA91013	Human pro
915	37.5	42.1	117	6	AD55314	Human pro
916	37.5	42.1	117	8	ADM87374	Human pro
917	37.5	42.1	226	3	AA34827	Gene 17 h
918	37.5	42.1	243	4	ABG17504	Novel hum
919	37.5	42.1	265	6	ABR43217	Human IRA
920	37.5	42.1	308	6	ABR43223	Human asp
921	37.5	42.1	743	8	ADU24126	Human dia
922	37.5	42.1	915	8	ABM84530	Human dia
923	37.5	42.1	917	8	ABM84529	Human dia
924	37.5	42.1	1076	8	ADS24798	Bacterial
925	37	41.6	5	4	AA90242	Factor VI
926	37	41.6	10	2	AA50921	Cyclic pe
927	37	41.6	10	2	AA50899	Cyclic pe
928	37	41.6	16	8	ADS33348	CMET-HGF
929	37	41.6	33	2	AA293328	HDX prote
930	37	41.6	38	4	AA18829	Peptide #
931	37	41.6	38	4	AB37939	Peptide #
932	37	41.6	38	4	AA31349	Peptide #
933	37	41.6	38	4	AB23191	Protein #
934	37	41.6	38	4	AA71072	Human bon
935	37	41.6	38	4	AA58571	Human bra
936	37	41.6	38	4	ABG52787	Human liv
937	37	41.6	38	5	ABG40865	Human pep
938	37	41.6	44	4	AA85762	Human imm
939	37	41.6	46	3	AA51398	Human sec
940	37	41.6	46	4	AB38221	Peptide #
941	37	41.6	46	4	AA31652	Peptide #
942	37	41.6	46	4	AA23403	Protein #
943	37	41.6	46	4	AA71371	Human bon
944	37	41.6	46	4	AA58854	Human bra
945	37	41.6	46	4	AB53076	Human liv
946	37	41.6	46	4	ABG41172	Human pep
947	37	41.6	46	5	ABG41172	Polypepti
948	37	41.6	48	7	ADD44528	Propionib
949	37	41.6	50	4	AAU64299	Propionib
950	37	41.6	50	6	ABM60818	Human nov
951	37	41.6	54	4	AAU21563	Human gen
952	37	41.6	55	4	AAE01567	Human alb
953	37	41.6	55	5	ABG63789	Albumin f
954	37	41.6				

974 37 41.6 110 3 AAY87227 Human sig
975 37 41.6 118 7 ABO71567 Pseudomon
976 37 41.6 118 7 ABO72444 Pseudomon
977 37 41.6 119 8 ADR08634 Human pro
978 37 41.6 121 7 ABO81199 Pseudomon
979 37 41.6 125 2 AAW29330 A partial
980 37 41.6 131 4 ABG27769 Novel hum
981 37 41.6 136 5 ABP42783 Human ova
982 37 41.6 143 4 AAU17510 Novel sig
983 37 41.6 143 4 AAM85152 Human imm
984 37 41.6 143 5 ABP42149 Human ova
985 37 41.6 143 5 ABO27214 Human sig
986 37 41.6 143 7 ADB94218 Human nov
987 37 41.6 145 4 AAE01652 Human gen
988 37 41.6 145 4 ABO11654 Human MDD
989 37 41.6 150 6 ABO03063 Human exp
990 37 41.6 154 4 AAU20337 Human nov
991 37 41.6 155 2 AAY36619 Fragment
992 37 41.6 155 6 ADA11789 Human nov
993 37 41.6 160 4 ABG26487 Novel hum
994 37 41.6 168 2 AAY41225 M. Polymo
995 37 41.6 172 4 AAU63930 Propionib
996 37 41.6 172 6 ABM60449 Propionib
997 37 41.6 172 6 ABU41718 Protein e
998 37 41.6 173 4 AAE01655 Human gen
999 37 41.6 179 7 ABO75761 Pseudomon
1000 37 41.6 180 7 ABO69523 Pseudomon

ALIGNMENTS

RESULT 1
AAB90146
ID AAB90146 standard; peptide; 13 AA.
XX AC AAB90146;
XX 23-MAY-2001 (first entry)
XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 4.
XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thrombembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
KW septicaemia; hypotension; angioedema; ARDS.
XX Synthetic.
XX WO200110892-A2.
XX 15-FEB-2001.
XX 04-AUG-2000; 2000WO-US021296.
XX 06-AUG-1999; 99US-0147627P.
XX 23-AUG-1999; 99US-0150315P.
XX (GETH) GENENTECH INC.
XX Dennis MS;
XX WPI; 2001-211069/21.
XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.
XX Claim 1; Page 49; 80pp; English.
XX This invention relates to peptides which act as antagonist of Factor VIIa
CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation

CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
CC activity in the presence of a tissue factor (TF) and for treating a
CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
CC treated include chronic thrombembolic diseases or disorders associated
CC with fibrin formation including vascular disorders such as deep venous
CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
CC arteriosclerosis and restenosis following angioplasty, acute and chronic
CC indications such as inflammation, septic shock, septicaemia, hypotension,
CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
CC and other diseases like inflammatory disorders. The antagonist peptides
CC are also useful in research, and for diagnostic, therapeutic and
CC prophylactic purposes. The present sequence represents a factor VIIa
CC antagonist peptide of the invention
XX
XX Sequence 13 AA;
Query Match 100.0%; Score 89; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13
RESULT 2
AAB82342
ID ABR82342 standard; peptide; 13 AA.
XX AC ABR82342;
XX 06-NOV-2003 (first entry)
XX Factor X activation inhibiting A-series peptide A-65.
XX Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
KW factor X.
XX Synthetic.
XX WO2003060463-A2.
XX 24-JUL-2003.
XX 30-JUL-2002; 2002WO-US024216.
XX 30-JUL-2001; 2001US-0308790P.
XX 20-AUG-2001; 2001US-0313608P.
XX 21-AUG-2001; 2001US-0313854P.
XX 14-SEP-2001; 2001US-0322227P.
XX (PURD) PURDUE RES FOUND.
XX (PITT/) PITTDENDRIGH B R.
XX (MURD/) MURDOCK L L.
XX (GAFF/) GAFFNEY P J.
XX Pittendriugh BR, Murdock LL, Gaffney PJ;
XX WPI; 2003-598567/56.
XX Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.
XX Example; Fig 24; 124pp; English.
XX The invention relates to evaluating the efficacy of molecule against a
CC target population including a pest strain resistant to first toxin. The
CC method involves determining pest strain susceptible to the first toxin, of
CC selecting strain resistant to first toxin, and evaluating the efficacy of
CC resistant strain with molecules to determine second toxin that is more

CC toxic to resistant strain than to susceptible strain. The resistant and
CC susceptible strains co-exist in the target population. The method is
CC useful for evaluating the efficacy of molecule against a target
CC population comprising pest strain resistant to first toxin, e.g. insect
CC population, mammalian population, plant population, animal population, or
CC virus population. The efficacy of molecules to kill unwanted resistant
CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
CC that inhibit the activation of factor X
XX
XX Sequence 13 AA;

Query Match 100.0%; Score 89; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13

RESULT 3
ADM96618
ID ADM96618 standard; peptide; 13 AA.

AC ADM96618;

XX 29-JUL-2004 (first entry)

XX Tissue factor VIIa (tFVIIa) peptide antagonist #40.

XX Tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
KW fibrin formation; vascular disorders; deep venous thrombosis;
KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX Synthetic.

XX US2004087767-A1.

XX 06-MAY-2004.

XX 30-JAN-2003; 2003US-00356257.

XX 06-FEB-2002; 2002US-0355420P.

XX (GETH) GENENTECH INC.

XX Lazarus RA, Maun HR;

XX WPI; 2004-356247/33.

XX New peptide, useful for preventing or treating chronic thromboembolic
PT diseases or disorders associated with fibrin formation including vascular
PT disorders, such as deep venous thrombosis, arterial thrombosis, and
PT stroke.

XX Disclosure; SEQ ID NO 40; 102pp; English.

XX The invention relates to peptide antagonists of tissue Factor VIIa
CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
CC with the peptide in the presence of tissue factor and under conditions
CC that allow binding of the compound to FVIIa to occur. The peptides are
CC useful for preventing or treating chronic thromboembolic diseases or
CC disorders associated with fibrin formation including vascular disorders,
CC such as deep venous thrombosis, arterial thrombosis, stroke,
CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
CC peptide antagonist of the invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 89; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13

RESULT 4

AAB90165

ID AAB90165 standard; peptide; 15 AA.

AC AAB90165;

XX 23-MAY-2001 (first entry)

XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 23.

XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thromboembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; atherosclerosis; restenosis; inflammation; septic shock;
KW septicaemia; hypotension; angioedema; ARDS.

XX Synthetic.

XX WO200110892-A2.

XX 15-FEB-2001.

XX 04-AUG-2000; 2000WO-US021296.

XX 06-AUG-1999; 99US-0147627P.

XX 23-AUG-1999; 99US-0150315P.

XX (GETH) GENENTECH INC.

XX Dennis MS;

XX WPI; 2001-211069/21.

XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
PT blocks initial events of blood coagulation.

XX Example 1; Fig 4; 80pp; English.

XX This invention relates to peptides which act as antagonist of Factor VIIa
CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
CC activity in the presence of a tissue factor (TF) and for treating a
CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
CC treated include chronic thromboembolic diseases or disorders associated
CC with fibrin formation including vascular disorders such as deep venous
CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
CC atherosclerosis and restenosis following angioplasty, acute and chronic
CC indications such as inflammation, septic shock, septicaemia, hypotension,
CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
CC and other diseases like inflammatory disorders. The antagonist peptides
CC are also useful in research, and for diagnostic, therapeutic and
CC prophylactic purposes. The present sequence represents a factor VIIa
CC antagonist peptide of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 5

ABR82341
ID ABR82341 standard; peptide; 15 AA.
XX
AC ABR82341;
XX
XX 06-NOV-2003 (first entry)
DT
DE Factor X activation inhibiting A-series peptide A-183.
XX
XX Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
KW factor X.
XX
XX Synthetic.
OS
XX WO2003060463-A2.
PN
XX 24-JUL-2003.
PD
XX 30-JUL-2002; 2002WO-US024216.
PF
XX 30-JUL-2001; 2001US-0308790P.
PR
XX 20-AUG-2001; 2001US-0313608P.
PR
XX 21-AUG-2001; 2001US-0313854P.
PR
XX 14-SEP-2001; 2001US-0322227P.
PR
XX (PURD) PURDUE RES FOUND.
PA (PITT/) PITTEDRIGH B R.
PA (MURD/) MURDOCK L L.
PA (GAFF/) GAFFNEY P J.
XX
XX Pittendrigh BR, Murdock LL, Gaffney PU;
PI
XX WPI; 2003-598567/56.
DR
XX
XX Evaluating the efficacy of molecule against target population including
PT toxin-resistant pest strain, by determining susceptible pest strain,
PT selecting resistant strain, and evaluating efficacy of resistant strain
PT with molecules.
PT
XX Example; Fig 24; 124pp; English.
PS
XX
XX The invention relates to evaluating the efficacy of molecule against a
CC target population including a pest strain resistant to first toxin. The
CC method involves determining pest strain susceptible to the first toxin,
CC selecting strain resistant to first toxin, and evaluating the efficacy of
CC resistant strain with molecules to determine second toxin that is more
CC toxic to resistant strain than to susceptible strain. The resistant and
CC susceptible strains co-exist in the target population. The method is
CC useful for evaluating the efficacy of molecule against a target
CC population comprising pest strain resistant to first toxin, e.g. insect
CC population, mammalian population, plant population, animal population, or
CC virus population. The efficacy of molecules to kill unwanted resistant
CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
CC that inhibit the activation of factor X
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 89; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15
RESULT 6
ADM96610
ID ADM96610 standard; peptide; 15 AA.
XX
AC ADM96610;
XX
XX 29-JUL-2004 (first entry)
DT

XX Tissue factor VIIa (tFVIIa) peptide antagonist #32.
DE
XX Tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
KW fibrin formation; vascular disorders; deep venous thrombosis;
KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX
OS Synthetic.
XX US2004087767-A1.
PN
XX 06-MAY-2004.
PD
XX 30-JAN-2003; 2003US-00356257.
PF
XX 06-FEB-2002; 2002US-0355420P.
PR
XX (GETH) GENENTECH INC.
PA
XX Lazarus RA, Maun HR;
PI
XX WPI; 2004-356247/33.
DR
XX
XX New peptide, useful for preventing or treating chronic thromboembolic
PT diseases or disorders associated with fibrin formation including vascular
PT disorders, such as deep venous thrombosis, arterial thrombosis, and
PT stroke.
PT
XX Disclosure; SEQ ID NO 32; 102pp; English.
PS
XX
XX The invention relates to peptide antagonists of tissue Factor VIIa
CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
CC with the peptide in the presence of tissue factor and under conditions
CC that allow binding of the compound to FVIIa to occur. The peptides are
CC useful for preventing or treating chronic thromboembolic diseases or
CC disorders associated with fibrin formation including vascular disorders,
CC such as deep venous thrombosis, arterial thrombosis, stroke,
CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
CC peptide antagonist of the invention.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13
RESULT 7
ADM96581
ID ADM96581 standard; peptide; 15 AA.
XX
AC ADM96581;
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Tissue factor VIIa (tFVIIa) peptide antagonist #3.
DE
XX Tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
KW fibrin formation; vascular disorders; deep venous thrombosis;
KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX
OS Synthetic.
XX US2004087767-A1.
PN
XX 06-MAY-2004.
PD
XX 30-JAN-2003; 2003US-00356257.
PF
XX

Read date

Read date

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 10
AAB90159
ID AAB90159 standard; peptide; 16 AA.
XX AC
XX AAB90159;
XX 23-MAY-2001 (first entry)
XX DE
XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 17.
XX KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX KW chronic thrombembolic disease; fibrin formation; vascular disorder;
XX KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX KW septicemia; hypotension; angioedema; ARDS.
XX OS Synthetic.
XX PN WO200110892-A2.
XX PD 15-FEB-2001.
XX PF 04-AUG-2000; 2000WO-US021296.
XX PR 06-AUG-1999; 99US-0147627P.
XX PR 23-AUG-1999; 99US-0150315P.
XX PA (GETH) GENENTECH INC.
XX PI Dennis MS;
XX PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
XX PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
XX PT blocks initial events of blood coagulation.
XX PS Example 1; Fig 4; 80pp; English.
XX CC This invention relates to peptides which act as antagonist of Factor VIIa
XX CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX CC activity in the presence of a tissue factor (TF) and for treating a
XX CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX CC treated include chronic thrombembolic diseases or disorders associated
XX CC with fibrin formation including vascular disorders such as deep venous
XX CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX CC arteriosclerosis and restenosis following angioplasty, acute and chronic
XX CC indications such as inflammation, septic shock, septicemia, hypotension,
XX CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
XX CC and other diseases like inflammatory disorders. The antagonist peptides
XX CC are also useful in research, and for diagnostic, therapeutic and
XX CC prophylactic purposes. The present sequence represents a factor VIIa
XX CC antagonist peptide of the invention
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 2 WEVLCWTWETCER 14

RESULT 11
ABR82340
ID ABR82340 standard; peptide; 16 AA.
XX AC
XX ABR82340;
XX DT
XX 06-NOV-2003 (first entry)
XX DE Factor X activation inhibiting A-series peptide A-99.
XX KW Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
XX KW factor X.
XX OS Synthetic.
XX PN WO2003060463-A2.
XX PD 24-JUL-2003.
XX PF 30-JUL-2002; 2002WO-US024216.
XX PR 30-JUL-2001; 2001US-0308790P.
XX PR 20-AUG-2001; 2001US-0313608P.
XX PR 21-AUG-2001; 2001US-0313854P.
XX PR 14-SEP-2001; 2001US-0322277P.
XX PA (PURD) PURDUE RES FOUND.
XX PA (PITT/) PITTDENDRIGH B R.
XX PA (MURD/) MURDOCK L L.
XX PA (GAFF/) GAFFNEY P J.
XX PI Pittendriugh BR, Murdock LL, Gaffney PJ;
XX DR WPI; 2003-598567/56.
XX CC Evaluating the efficacy of molecule against target population including
XX CC toxin-resistant pest strain, by determining susceptible pest strain,
XX CC selecting resistant strain, and evaluating efficacy of resistant strain
XX CC with molecules.
XX PS Example; Fig 24; 124pp; English.
XX CC The invention relates to evaluating the efficacy of molecule against a
XX CC target population including a pest strain resistant to first toxin. The
XX CC method involves determining pest strain susceptible to the first toxin,
XX CC selecting strain resistant to first toxin, and evaluating the efficacy of
XX CC resistant strain with molecules to determine second toxin that is more
XX CC toxic to resistant strain than to susceptible strain. The resistant and
XX CC susceptible strains co-exist in the target population. The method is
XX CC useful for evaluating the efficacy of molecule against a target
XX CC population comprising pest strain resistant to first toxin, e.g. insect
XX CC population, mammalian population, plant population, animal population, or
XX CC virus population. The efficacy of molecules to kill unwanted resistant
XX CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
XX CC that inhibit the activation of factor X
XX SQ Sequence 16 AA;

Query Match 100.0%; Score 89; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 2 WEVLCWTWETCER 14

RESULT 12
AAB90160
ID AAB90160 standard; peptide; 18 AA.
XX AC
XX AAB90160;
XX XX

DT 23-MAY-2001 (first entry)
 DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 18.
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX Synthetic.
 OS
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX 04-AUG-2000; 2000WO-US021296.
 PF
 XX 06-AUG-1999; 99US-0147627P.
 PR 23-AUG-1999; 99US-0150315P.
 XX (GETH) GENENTECH INC.
 PA
 XX Dennis MS;
 PI
 XX WPI; 2001-211069/21.
 DR
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX Example 1; Fig 4; 80pp; English.
 PS
 XX This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thrombembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWTWETCER 15
 |||||
 RESULT 13
 ABR82338
 ID ABR82338 standard; peptide; 18 AA.
 XX
 AC ABR82338;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Factor X activation inhibiting A-series peptide A-100-Z.
 KW Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
 KW factor X.
 XX
 XX Synthetic.
 OS
 XX WO2003060463-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 30-JUL-2002; 2002WO-US024216.
 PF
 XX 30-JUL-2001; 2001US-0308790P.
 PR 20-AUG-2001; 2001US-0313608P.
 PR 21-AUG-2001; 2001US-0313854P.
 PR 14-SEP-2001; 2001US-0322227P.
 XX (PURD) PURDUE RES FOUND.
 PA (PITT/) PURDUE DRUG CO.
 PA (MURD/) MURDOCK L L.
 PA (GAFF/) GAFFNEY P J.
 XX Pittendriigh BR, Murdock LL, Gaffney PJ;
 PI
 XX WPI; 2003-598567/56.
 DR
 XX Evaluating the efficacy of molecule against target population including
 PT toxin-resistant pest strain, by determining susceptible pest strain,
 PT selecting resistant strain, and evaluating efficacy of resistant strain
 PT with molecules.
 XX Example; Fig 24; 124pp; English.
 PS
 XX The invention relates to evaluating the efficacy of molecule against a
 CC target population including a pest strain resistant to first toxin. The
 CC method involves determining pest strain susceptible to the first toxin.
 CC selecting strain resistant to first toxin, and evaluating the efficacy of
 CC resistant strain with molecules to determine second toxin that is more
 CC toxic to resistant strain than to susceptible strain. The resistant and
 CC susceptible strains co-exist in the target population. The method is
 CC useful for evaluating the efficacy of molecule against a target
 CC population comprising pest strain resistant to first toxin, e.g. insect
 CC population, mammalian population, plant population, animal population, or
 CC virus population. The efficacy of molecules to kill unwanted resistant
 CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
 CC that inhibit the activation of factor X
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 89; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWTWETCER 15
 |||||
 RESULT 14
 ABR82339
 ID ABR82339 standard; peptide; 18 AA.
 XX
 AC ABR82339;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Factor X activation inhibiting A-series peptide A-100.
 KW Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
 KW factor X.
 XX
 XX Synthetic.
 OS
 XX WO2003060463-A2.
 PN
 XX 24-JUL-2003.
 PD

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XX PF 30-JUL-2002; 2002WO-US024216.
XX PR 30-JUL-2001; 2001US-0308790P.
XX PR 20-AUG-2001; 2001US-0313608P.
XX PR 21-AUG-2001; 2001US-0313854P.
XX PR 14-SEP-2001; 2001US-032227P.
XX PR (PURD ) PURDUE RES FOUND.
XX PA (PITT/) PITTEDRIGH B R.
XX PA (MURD/) MURDOCK L L.
XX PA (GAFF/) GAFFNEY P J.
XX PI Pittendrigh BR, Murdock LL, Gaffney PJ;
XX XX WPI; 2003-598567/56.
XX XX Evaluating the efficacy of molecule against target population including
XX PT toxin-resistant pest strain, by determining susceptible pest strain,
XX PT selecting resistant strain, and evaluating efficacy of resistant strain
XX PT with molecules.
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XX CC selecting strain resistant to first toxin, and evaluating the efficacy of
XX CC resistant strain with molecules to determine second toxin that is more
XX CC toxic to resistant strain than to susceptible strain. The resistant and
XX CC susceptible strains co-exist in the target population. The method is
XX CC useful for evaluating the efficacy of molecule against a target
XX CC population comprising pest strain resistant to first toxin, e.g. insect
XX CC population, mammalian population, plant population, animal population, or
XX CC virus population. The efficacy of molecules to kill unwanted resistant
XX CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
XX CC that inhibit the activation of factor X
XX SQ Sequence 18 AA;
XX Query Match 100.0%; Score 89; DB 6; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-05;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWTETCER 13
Db |||||
3 WEVLCTWTETCER 15

RESULT 15
ABR82337
ID ABR82337 standard; peptide; 20 AA.
XX AC ABR82337;
XX XX 06-NOV-2003 (first entry)
XX DT Factor X activation inhibiting A-series peptide C-Z.
XX DE Soyastatin N; scN; cystatin; negative cross resistance toxin; NCR;
XX KW factor X.
XX OS Synthetic.
XX OS WO2003060463-A2.
XX PN 24-JUL-2003.
XX PD 30-JUL-2002; 2002WO-US024216.
XX PF 30-JUL-2001; 2001US-0308790P.
XX PR 20-AUG-2001; 2001US-0313608P.
XX PR 21-AUG-2001; 2001US-0313854P.
XX PI (GETH ) GENENTECH INC.
Dennis MS;

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PR 14-SEP-2001; 2001US-032227P.
XX (PURD ) PURDUE RES FOUND.
XX PA (PITT/) PITTEDRIGH B R.
XX PA (MURD/) MURDOCK L L.
XX PA (GAFF/) GAFFNEY P J.
XX PI Pittendrigh BR, Murdock LL, Gaffney PJ;
XX XX WPI; 2003-598567/56.
XX XX Evaluating the efficacy of molecule against target population including
XX PT toxin-resistant pest strain, by determining susceptible pest strain,
XX PT selecting resistant strain, and evaluating efficacy of resistant strain
XX PT with molecules.
XX PS Example; Fig 24; 124pp; English.
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XX CC method involves determining pest strain susceptible to the first toxin,
XX CC selecting strain resistant to first toxin, and evaluating the efficacy of
XX CC resistant strain with molecules to determine second toxin that is more
XX CC toxic to resistant strain than to susceptible strain. The resistant and
XX CC susceptible strains co-exist in the target population. The method is
XX CC useful for evaluating the efficacy of molecule against a target
XX CC population comprising pest strain resistant to first toxin, e.g. insect
XX CC population, mammalian population, plant population, animal population, or
XX CC virus population. The efficacy of molecules to kill unwanted resistant
XX CC organisms is increased. Sequences ABR82336-49 represent A-series peptides
XX CC that inhibit the activation of factor X
XX SQ Sequence 20 AA;
XX Query Match 100.0%; Score 89; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCTWTETCER 13
Db |||||
4 WEVLCTWTETCER 16

RESULT 16
AAB90199
ID AAB90199 standard; peptide; 22 AA.
XX AC AAB90199;
XX XX 23-MAY-2001 (first entry)
XX DT Factor VIIa (FVIIa) antagonist peptide SEQ ID 57.
XX DE Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX KW chronic thrombotic disease; fibrin formation; vascular disorder;
XX KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX KW septicaemia; hypotension; angioedema; ARDS.
XX OS Synthetic.
XX OS WO200110892-A2.
XX PN 15-FEB-2001.
XX PD 04-AUG-2000; 2000WO-US021296.
XX PF 06-AUG-1999; 99US-0147627P.
XX PR 23-AUG-1999; 99US-0150315P.
XX XX (GETH ) GENENTECH INC.
XX XX Dennis MS;
PI

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XX WPI; 2001-211069/21.
 XX
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX
 XX Example 1; Fig 4; 80pp; English.
 XX
 XX This invention relates to peptides which act as antagonist of Factor VIIa
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 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thrombotic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 XX Sequence 22 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB |||||
 1 WEVLCWTWETCER 13
 RESULT 17
 AAB90182
 ID AAB90182 standard; peptide; 24 AA.
 XX
 XX AAB90182;
 XX
 XX 23-MAY-2001 (first entry)
 XX
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 40.
 DE
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombotic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX
 XX Synthetic.
 OS
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX 04-AUG-2000; 2000WO-US021296.
 PF
 XX 06-AUG-1999; 99US-0147627P.
 PR
 XX 23-AUG-1999; 99US-0150315P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Dennis MS;
 PI
 XX WPI; 2001-211069/21.
 XX
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
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 XX

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 XX
 XX This invention relates to peptides which act as antagonist of Factor VIIa
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 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thrombotic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 XX Sequence 24 AA;
 SQ
 Query Match 100.0%; Score 89; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB |||||
 3 WEVLCWTWETCER 15
 RESULT 18
 AAB90181
 ID AAB90181 standard; peptide; 24 AA.
 XX
 XX AAB90181;
 XX
 XX 23-MAY-2001 (first entry)
 XX
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 39.
 DE
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombotic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX
 XX Synthetic.
 OS
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX 04-AUG-2000; 2000WO-US021296.
 PF
 XX 06-AUG-1999; 99US-0147627P.
 PR
 XX 23-AUG-1999; 99US-0150315P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Dennis MS;
 PI
 XX WPI; 2001-211069/21.
 XX
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
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 XX

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 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 89; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
 Db 3 WEVLCWTWETCER 15

RESULT 19
 AAB90183
 ID AAB90183 standard; peptide; 24 AA.

XX
 AC AAB90183;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 41.
 XX
 KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.

XX Synthetic.
 XX WO200110892-A2.
 XX 15-FEB-2001.

XX 04-AUG-2000; 2000WO-US021296.
 XX 06-AUG-1999; 99US-0147627P.
 XX 23-AUG-1999; 99US-0150315P.

XX (GETH) GENENTECH INC.

XX Dennis MS;

XX WPI; 2001-211069/21.

XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
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 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic

CC indications such as inflammation, septic shock, septicaemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 89; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
 Db 3 WEVLCWTWETCER 15

RESULT 20
 AAB90169
 ID AAB90169 standard; peptide; 24 AA.

XX AAB90169;

XX 23-MAY-2001 (first entry)

XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 27.

XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.

XX Synthetic.

XX WO200110892-A2.

XX 15-FEB-2001.

XX 04-AUG-2000; 2000WO-US021296.

XX 06-AUG-1999; 99US-0147627P.

XX 23-AUG-1999; 99US-0150315P.

XX (GETH) GENENTECH INC.

XX Dennis MS;

XX WPI; 2001-211069/21.

XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
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 PT blocks initial events of blood coagulation.

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 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicaemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa

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CC antagonist peptide of the invention
XX
SQ Sequence 24 AA;

Query Match      100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
   |||||
DB 3 WEVLCWTWETCER 15

RESULT 22
AAB90161
ID AAB90161 standard; peptide; 24 AA.
XX AC
XX AAB90161;
XX
DT 23-MAY-2001 (first entry)
XX
DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 19.
XX
KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thrombembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
KW septicemia; hypotension; angioedema; ARDS.
XX
OS Synthetic.
XX
PN WO200110892-A2.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000WO-US021296.
XX
PR 06-AUG-1999; 99US-0147627P.
XX
PR 23-AUG-1999; 99US-0150315P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Dennis MS;
XX
WPI; 2001-211069/21.

New factor VIIa antagonist peptide for research, diagnostic, therapeutic
and prophylactic methods, inhibits FVII/FVIIa mediated processes and
blocks initial events of blood coagulation.

Example 1; Fig 4; 80pp; English.

This invention relates to peptides which act as antagonist of Factor VIIa
(FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
activity in the presence of a tissue factor (TF) and for treating a
TF/FVIIa mediated disease or disorder in a host. Diseases which can be
treated include chronic thrombembolic diseases or disorders associated
with fibrin formation including vascular disorders such as deep venous
thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
arteriosclerosis and restenosis following angioplasty, acute and chronic
indications such as inflammation, septic shock, septicemia, hypotension,
cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
and other diseases like inflammatory disorders. The antagonist peptides
are also useful in research, and for diagnostic, therapeutic and
prophylactic purposes. The present sequence represents a factor VIIa
antagonist peptide of the invention

Sequence 24 AA;

Query Match      100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
   |||||
DB 3 WEVLCWTWETCER 15

RESULT 21
AAB90168
ID AAB90168 standard; peptide; 24 AA.
XX AC
XX AAB90168;
XX
DT 23-MAY-2001 (first entry)
XX
DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 26.
XX
KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
KW chronic thrombembolic disease; fibrin formation; vascular disorder;
KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
KW septicemia; hypotension; angioedema; ARDS.
XX
OS Synthetic.
XX
PN WO200110892-A2.
XX
PD 15-FEB-2001.
XX
PF 04-AUG-2000; 2000WO-US021296.
XX
PR 06-AUG-1999; 99US-0147627P.
XX
PR 23-AUG-1999; 99US-0150315P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Dennis MS;
XX
WPI; 2001-211069/21.

New factor VIIa antagonist peptide for research, diagnostic, therapeutic
and prophylactic methods, inhibits FVII/FVIIa mediated processes and
blocks initial events of blood coagulation.

Example 1; Fig 4; 80pp; English.

This invention relates to peptides which act as antagonist of Factor VIIa
(FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
activity in the presence of a tissue factor (TF) and for treating a
TF/FVIIa mediated disease or disorder in a host. Diseases which can be
treated include chronic thrombembolic diseases or disorders associated
with fibrin formation including vascular disorders such as deep venous
thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
arteriosclerosis and restenosis following angioplasty, acute and chronic
indications such as inflammation, septic shock, septicemia, hypotension,
cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
and other diseases like inflammatory disorders. The antagonist peptides
are also useful in research, and for diagnostic, therapeutic and
prophylactic purposes. The present sequence represents a factor VIIa
antagonist peptide of the invention

Sequence 24 AA;

Query Match      100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
   |||||
DB 3 WEVLCWTWETCER 15

```

RESULT 23
ADM96595
ID ADM96595 standard; peptide; 15 AA.
XX AC ADM96595;
XX DT 29-JUL-2004 (first entry)
XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #17.
XX KW Tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;
XX KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX OS Synthetic.
XX PN US2004087767-A1.
XX PD 06-MAY-2004.
XX PF 30-JAN-2003; 2003US-00356257.
XX PR 06-FEB-2002; 2002US-0355420P.
XX PA (GETH) GENENTECH INC.
XX PI Lazarus RA, Maun HR;
XX PT WPI; 2004-356247/33.
XX PT New peptide, useful for preventing or treating chronic thromboembolic
XX PT diseases or disorders associated with fibrin formation including vascular
XX PT disorders, such as deep venous thrombosis, arterial thrombosis, and
XX PT stroke.
XX PS Disclosure; SEQ ID NO 17; 102pp; English.
XX CC The invention relates to peptide antagonists of tissue Factor VIIa
XX CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
XX CC with the peptide in the presence of tissue factor and under conditions
XX CC that allow binding of the compound to FVIIa to occur. The peptides are
XX CC useful for preventing or treating chronic thromboembolic diseases or
XX CC disorders associated with fibrin formation including vascular disorders,
XX CC such as deep venous thrombosis, arterial thrombosis, stroke,
XX CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
XX CC peptide antagonist of the invention.
XX SQ Sequence 15 AA;
Query Match 98.9%; Score 88; DB 8; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.9e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15
RESULT 24
AAB90184
ID AAB90184 standard; peptide; 24 AA.
XX AC AAB90184;
XX XX
XX DT 23-MAY-2001 (first entry)
XX DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 42.
XX KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX KW chronic thromboembolic disease; fibrin formation; vascular disorder;
XX KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;

KW septicaemia; hypotension; angioedema; ARDS.
OS Synthetic.
XX WO200110892-A2.
XX FN 15-FEB-2001.
XX PD 04-AUG-2000; 2000WO-US021296.
XX PF 06-AUG-1999; 99US-0147627P.
XX PR 23-AUG-1999; 99US-0150315P.
XX XX (GETH) GENENTECH INC.
XX XX Dennis MS;
XX PI WPI; 2001-211069/21.
XX DR New factor VIIa antagonist peptide for research, diagnostic, therapeutic
XX XX and prophylactic methods, inhibits FVII/FVIIa mediated processes and
XX PT blocks initial events of blood coagulation.
XX PT Example 1; Fig 4; 80pp; English.
XX PS This invention relates to peptides which act as antagonist of Factor VIIa
XX CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX CC activity in the presence of a tissue factor (TF) and for treating a
XX CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX CC treated include chronic thromboembolic diseases or disorders associated
XX CC with fibrin formation including vascular disorders such as deep venous
XX CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX CC arteriosclerosis and restenosis following angioplasty, acute and chronic
XX CC indications such as inflammation, septic shock, septicaemia, hypotension,
XX CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
XX CC and other diseases like inflammatory disorders. The antagonist peptides
XX CC are also useful in research, and for diagnostic, therapeutic and
XX CC prophylactic purposes. The present sequence represents a factor VIIa
XX CC antagonist peptide of the invention
XX SQ Sequence 24 AA;
Query Match 98.9%; Score 88; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 3.1e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15
RESULT 25
ADM96596
ID ADM96596 standard; peptide; 15 AA.
XX AC ADM96596;
XX XX
XX DT 29-JUL-2004 (first entry)
XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #18.
XX KW Tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;
XX KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX OS Synthetic.
XX PN US2004087767-A1.
XX PD 06-MAY-2004.

PF 30-JAN-2003; 2003US-00356257.
 PR 06-FEB-2002; 2002US-0355420P.
 XX (GETH) GENENTECH INC.
 XX Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.
 DR New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX Disclosure; SEQ ID NO 18; 102pp; English.
 PS
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 97.8%; Score 87; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 2.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB 3 WEVNCWTWETCER 15
 |||:|||||||
 |||:|||||||
 RESULT 27
 AAB90185
 ID AAB90185 standard; peptide; 24 AA.
 XX
 AC AAB90185;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 43.
 XX
 KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thromboembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX
 OS Synthetic.
 XX
 PN WO200110892-A2.
 XX
 PD 15-FEB-2001.
 XX
 PF 04-AUG-2000; 2000WO-US021296.
 XX
 PR 06-AUG-1999; 99US-0147627P.
 XX
 PR 23-AUG-1999; 99US-0150315P.
 XX
 FA (GETH) GENENTECH INC.
 XX
 XX Dennis MS;
 XX PI
 XX WPI; 2001-211069/21.
 DR
 XX
 PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX
 PS Example 1; Fig 4; 80pp; English.
 XX
 CC This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thromboembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory

PF 30-JAN-2003; 2003US-00356257.
 PR 06-FEB-2002; 2002US-0355420P.
 XX (GETH) GENENTECH INC.
 XX Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.
 DR New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX Disclosure; SEQ ID NO 18; 102pp; English.
 PS
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 97.8%; Score 87; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 2.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB 3 WEVNCWTWETCER 15
 |||:|||||||
 |||:|||||||
 RESULT 26
 ADM96597
 ID ADM96597 standard; peptide; 15 AA.
 XX
 AC ADM96597;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #19.
 XX
 KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicemia.
 XX
 OS Synthetic.
 XX
 PN US2004087767-A1.
 XX
 PD 06-MAY-2004.
 XX
 XX 30-JAN-2003; 2003US-00356257.
 XX
 PR 06-FEB-2002; 2002US-0355420P.
 XX
 FA (GETH) GENENTECH INC.
 XX
 XX Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.
 DR New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX

XX

QY 1 WEVLCWTWETCER 13
 DB 1 WEVVCWTWETCER 13

RESULT 30

ADM96605
 ID ADM96605 standard; peptide; 15 AA.

XX AC ADM96605;

XX DT 29-JUL-2004 (first entry)

XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #27.

XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX OS Synthetic.

XX US2004087767-A1.

XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.

XX PR 06-FEB-2002; 2002US-0355420P.

XX PA (GETH) GENENTECH INC.

XX PI Lazarus RA, Maun HR;

XX DR WPI; 2004-356247/33.

XX PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

XX PS Disclosure; SEQ ID NO 27; 102pp; English.

XX CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

XX SQ Sequence 15 AA;

Query Match 96.6%; Score 86; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 3.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWTWETCER 15

RESULT 31

ADM96598
 ID ADM96598 standard; peptide; 15 AA.

XX AC ADM96598;

XX DT 29-JUL-2004 (first entry)

XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #20.

XX

KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX OS Synthetic.

XX US2004087767-A1.

XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.

XX PR 06-FEB-2002; 2002US-0355420P.

XX PA (GETH) GENENTECH INC.

XX PI Lazarus RA, Maun HR;

XX DR WPI; 2004-356247/33.

XX PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

XX PS Disclosure; SEQ ID NO 20; 102pp; English.

XX CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

XX SQ Sequence 15 AA;

Query Match 96.6%; Score 86; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 3.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVVCWTWETCER 15

RESULT 32

ADM96606
 ID ADM96606 standard; peptide; 15 AA.

XX AC ADM96606;

XX DT 29-JUL-2004 (first entry)

XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #28.

XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX OS Synthetic.

XX US2004087767-A1.

XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.

XX PR 06-FEB-2002; 2002US-0355420P.

XX PA (GETH) GENENTECH INC.

XX Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.
 XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX Disclosure; SEQ ID NO 28; 102pp; English.
 XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (FVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX Sequence 15 AA;
 SQ
 Query Match 96.6%; Score 86; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 3.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB |||||:|||||
 3 WEVLCWTWETCEK 15
 RESULT 33
 AAB90194
 ID AAB90194 standard; peptide; 24 AA.
 AC AAB90194;
 XX 23-MAY-2001 (first entry)
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 52.
 DE Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thromboembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX Synthetic.
 OS WO200110892-A2.
 XX 15-FEB-2001.
 XX 04-AUG-2000; 2000WO-US021296.
 XX 06-AUG-1999; 99US-0147627P.
 XX 23-AUG-1999; 99US-0150315P.
 XX (GETH) GENENTECH INC.
 PA Dennis MS;
 XX WPI; 2001-211069/21.
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX Example 1; Fig 4; 80pp; English.
 XX This invention relates to peptides which act as antagonist of Factor VIIa

CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thromboembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX Sequence 24 AA;
 SQ
 Query Match 96.6%; Score 86; DB 4; Length 24;
 Best Local Similarity 92.3%; Pred. No. 5.7e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WEVLCWTWETCER 13
 DB |||||:|||||
 3 WEVLCWTWETCER 15
 RESULT 34
 AAB90187
 ID AAB90187 standard; peptide; 24 AA.
 AC AAB90187;
 XX 23-MAY-2001 (first entry)
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 45.
 DE Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thromboembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 XX Synthetic.
 OS WO200110892-A2.
 XX 15-FEB-2001.
 XX 04-AUG-2000; 2000WO-US021296.
 XX 06-AUG-1999; 99US-0147627P.
 XX 23-AUG-1999; 99US-0150315P.
 XX (GETH) GENENTECH INC.
 PA Dennis MS;
 XX WPI; 2001-211069/21.
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX Example 1; Fig 4; 80pp; English.
 XX This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thromboembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous

thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis, arteriosclerosis and restenosis following angioplasty, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC) and other diseases like inflammatory disorders. The antagonist peptides are also useful in research, and for diagnostic, therapeutic and prophylactic purposes. The present sequence represents a factor VIIa antagonist peptide of the invention

CC SQ Sequence 24 AA;

Query Match 96.6%; Score 86; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 5.7e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 35
AAB90195
ID AAB90195 standard; peptide; 24 AA.

XX AC AAB90195;

XX DT 23-MAY-2001 (first entry)

XX DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 53.

XX KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX KW chronic thromboembolic disease; fibrin formation; vascular disorder;
XX KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX KW septicemia; hypotension; angioedema; ARDS.

XX OS Synthetic.

XX PN WO200110892-A2.

XX PD 15-FEB-2001.

XX PF 04-AUG-2000; 2000WO-US021296.

XX PR 06-AUG-1999; 99US-0147627P.

XX PR 23-AUG-1999; 99US-0150315P.

XX PA (GETH) GENENTECH INC.

XX PI Dennis MS;

XX WPI; 2001-211069/21.

XX PT New factor VIIa antagonist peptide for research, diagnostic, therapeutic and prophylactic methods, inhibits FVII/FVIIa mediated processes and blocks initial events of blood coagulation.

XX PS Example 1; Fig 4; 80pp; English.

XX CC This invention relates to peptides which act as antagonist of Factor VIIa (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation factor. FVIIa antagonist peptides are useful for inhibiting FVIIa activity in the presence of a tissue factor (TF) and for treating a TF/FVIIa mediated disease or disorder in a host. Diseases which can be treated include chronic thromboembolic diseases or disorders associated with fibrin formation including vascular disorders such as deep venous thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis, arteriosclerosis and restenosis following angioplasty, acute and chronic indications such as inflammation, septic shock, septicemia, hypotension, cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC) and other diseases like inflammatory disorders. The antagonist peptides

CC are also useful in research, and for diagnostic, therapeutic and prophylactic purposes. The present sequence represents a factor VIIa antagonist peptide of the invention

CC SQ Sequence 24 AA;

Query Match 96.6%; Score 86; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 5.7e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 36
ADM96585
ID ADM96585 standard; peptide; 15 AA.

XX AC ADM96585;

XX DT 29-JUL-2004 (first entry)

XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #7.

XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;
XX KW arterial thrombosis; stroke; atherosclerosis; septicemia.

XX OS Synthetic.

XX PN US2004087767-A1.

XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.

XX PR 06-FEB-2002; 2002US-0355420P.

XX PA (GETH) GENENTECH INC.

XX PI Lazarus RA, Maun HR;

XX WPI; 2004-356247/33.

XX PT New peptide, useful for preventing or treating chronic thromboembolic diseases or disorders associated with fibrin formation including vascular disorders, such as deep venous thrombosis, arterial thrombosis, and stroke.

XX PS Disclosure; SEQ ID NO 7; 102pp; English.

XX CC The invention relates to peptide antagonists of tissue Factor VIIa (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa with the peptide in the presence of tissue factor and under conditions that allow binding of the compound to FVIIa to occur. The peptides are useful for preventing or treating chronic thromboembolic diseases or disorders associated with fibrin formation including vascular disorders, such as deep venous thrombosis, arterial thrombosis, stroke, atherosclerosis, or septicemia. The present sequence represents a tFVIIa peptide antagonist of the invention.

XX SQ Sequence 15 AA;

Query Match 95.5%; Score 85; DB 8; Length 15;
Best Local Similarity 92.3%; Pred. No. 5e-05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEALCWTWETCER 15

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RESULT 37
AAB90172
ID AAB90172 standard; peptide; 24 AA.
XX
XX AC AAB90172;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 30.
XX
XX KW Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
XX KW chronic thromboembolic disease; fibrin formation; vascular disorder;
XX KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
XX KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
XX KW septicemia; hypotension; angioedema; ARDS.
XX
XX OS Synthetic.
XX
XX PN WO200110892-A2.
XX
XX PD 15-FEB-2001.
XX
XX PF 04-AUG-2000; 2000WO-US021296.
XX
XX PR 06-AUG-1999; 99US-0147627P.
XX PR 23-AUG-1999; 99US-0150315P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Dennis MS;
XX
XX PT WPI; 2001-211069/21.
XX
XX DR New factor VIIa antagonist peptide for research, diagnostic, therapeutic
XX PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
XX PT blocks initial events of blood coagulation.
XX
XX PS Example 1; Fig 4; 80pp; English.
XX
XX CC This invention relates to peptides which act as antagonist of Factor VIIa
XX CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
XX CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
XX CC activity in the presence of a tissue factor (TF) and for treating a
XX CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
XX CC treated include chronic thromboembolic diseases or disorders associated
XX CC with fibrin formation including vascular disorders such as deep venous
XX CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
XX CC arteriosclerosis and restenosis following angioplasty, acute and chronic
XX CC indications such as inflammation, septic shock, septicemia, hypotension,
XX CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
XX CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
XX CC and other diseases like inflammatory disorders. The antagonist peptides
XX CC are also useful in research, and for diagnostic, therapeutic and
XX CC prophylactic purposes. The present sequence represents a factor VIIa
XX CC antagonist peptide of the invention
XX
XX SQ Sequence 24 AA;
XX
XX Query Match 95.5%; Score 85; DB 4; Length 24;
XX Best Local Similarity 92.3%; Pred. No. 7.9e-05;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEALCWTWETCER 15

RESULT 38
AAB92347
ID ABR82347 standard; peptide; 12 AA.
XX
XX AC ABR82347;
XX
XX KW Tissue factor VIIa (tFVIIa) peptide antagonist #26.
XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;

Qy 1 WEVLCWTWETCER 12
Db 1 WEVLCWTWETCER 12

RESULT 39
ADM96604
ID ADM96604 standard; peptide; 15 AA.
XX
XX AC ADM96604;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #26.
XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;

Qy 1 WEVLCWTWETCER 12
Db 1 WEVLCWTWETCER 12

Query Match 94.4%; Score 84; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
 XX Synthetic.
 OS
 XX US2004087767-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 XX 06-FEB-2002; 2002US-0355420P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Lazarus RA, Maun HR;
 PI
 XX WPI; 2004-356247/33.
 DR
 XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 PS Disclosure; SEQ ID NO 26; 102pp; English.
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 15 AA;
 XX

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWTWETCER 15

RESULT 40
 ADM96607
 ID ADM96607 standard; peptide; 15 AA.
 XX
 AC ADM96607;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #29.
 XX
 XX tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
 XX
 OS Synthetic.
 XX
 XX US2004087767-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 XX 06-FEB-2002; 2002US-0355420P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Lazarus RA, Maun HR;
 PI

XX WPI; 2004-356247/33.
 DR
 XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 PS Disclosure; SEQ ID NO 29; 102pp; English.
 XX
 CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 15 AA;
 XX

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 12
 DB 3 WEVLCWTWETCER 14

RESULT 41
 ADM96608
 ID ADM96608 standard; peptide; 15 AA.
 XX

AC ADM96608;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIa (tFVIIa) peptide antagonist #30.
 XX
 KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
 XX
 OS Synthetic.
 XX

XX US2004087767-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 XX 06-FEB-2002; 2002US-0355420P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Lazarus RA, Maun HR;
 PI
 XX WPI; 2004-356247/33.
 DR

XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX

PS Disclosure; SEQ ID NO 30; 102pp; English.
 XX

CC The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or

CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

XX
 SQ Sequence 15 AA;
 Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WEVLCWTWETCE 12
 |||||
 Db 3 WEVLCWTWETCE 14

RESULT 42
 ADM96593
 ID ADM96593 standard; peptide; 15 AA.

XX AC ADM96593;
 XX DT 29-JUL-2004 (first entry)
 XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #15.
 XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX OS Synthetic.
 XX FN US2004087767-A1.
 XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.
 XX PR 06-FEB-2002; 2002US-0355420P.
 XX PA (GETH) GENENTECH INC.

XX PI Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.

XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

XX Disclosure; SEQ ID NO 15; 102pp; English.

XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

XX Sequence 15 AA;

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WEVLCWTWETCE 12
 |||||
 Db 3 WEVLCWTWETCE 14

RESULT 43
 ADM96591
 ID ADM96591 standard; peptide; 15 AA.

XX AC ADM96591;
 XX DT 29-JUL-2004 (first entry)
 XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #13.

XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX OS Synthetic.
 XX FN US2004087767-A1.
 XX PD 06-MAY-2004.

XX PF 30-JAN-2003; 2003US-00356257.
 XX PR 06-FEB-2002; 2002US-0355420P.

XX PA (GETH) GENENTECH INC.
 XX PI Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.

XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.

XX Disclosure; SEQ ID NO 13; 102pp; English.

XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicaemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.

XX Sequence 15 AA;

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 WEVLCWTWETCE 13
 |||||
 Db 3 WEVLCWTWETCE 15

RESULT 44
 ADM96586
 ID ADM96586 standard; peptide; 15 AA.

XX AC ADM96586;
 XX DT 29-JUL-2004 (first entry)
 XX DE Tissue factor VIIa (tFVIIa) peptide antagonist #8.
 XX KW tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicaemia.

XX

OS Synthetic.
 XX US2004087767-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX 30-JAN-2003; 2003US-00356257.
 XX
 XX 06-FEB-2002; 2002US-0355420P.
 PR
 XX (GETH) GENENTECH INC.
 XX Lazarus RA, Maun HR;
 PI
 XX WPI; 2004-356247/33.
 DR
 XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX Disclosure; SEQ ID NO 8; 102pp; English.
 PS
 XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX Sequence 15 AA;
 SQ

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVACWTWETCER 15
 |||||

RESULT 45
 ADM96588
 ID ADM96588 standard; peptide; 15 AA.
 XX
 AC ADM96588;
 XX
 XX 29-JUL-2004 (first entry)
 DT
 XX Tissue factor VIIa (tFVIIa) peptide antagonist #10.
 DE
 XX tissue Factor VIIa; tFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicemia.
 KW
 XX Synthetic.
 OS
 XX US2004087767-A1.
 PN
 XX 06-MAY-2004.
 PD
 XX 30-JAN-2003; 2003US-00356257.
 XX
 XX 06-FEB-2002; 2002US-0355420P.
 PR
 XX (GETH) GENENTECH INC.
 XX Lazarus RA, Maun HR;
 PI
 XX WPI; 2004-356247/33.
 DR

XX New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX Disclosure; SEQ ID NO 10; 102pp; English.
 PS
 XX The invention relates to peptide antagonists of tissue Factor VIIa
 CC (tFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
 CC peptide antagonist of the invention.
 XX Sequence 15 AA;
 SQ

Query Match 94.4%; Score 84; DB 8; Length 15;
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWAWETCER 15
 |||||

RESULT 46
 AAB90196
 ID AAB90196 standard; peptide; 24 AA.
 XX
 AC AAB90196;
 XX
 XX 23-MAY-2001 (first entry)
 DT
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 54.
 DE
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thromboembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicemia; hypotension; angioedema; ARDS.
 KW
 XX Synthetic.
 OS
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX 04-AUG-2000; 2000WO-US021296.
 XX
 XX 06-AUG-1999; 99US-0147627P.
 PR
 XX 23-AUG-1999; 99US-0150315P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Dennis MS;
 PI
 XX WPI; 2001-211069/21.
 DR
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 PT
 XX Example 1; Fig 4; 80pp; English.
 PS
 XX This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be

CC treated include chronic thrombembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicaemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 SQ Sequence 24 AA;

Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 12
 DB 3 WEVLCWTWETCE 14

RESULT 47
 AAB90175
 ID AAB90175 standard; peptide; 24 AA.
 AC AAB90175;
 XX
 XX 23-MAY-2001 (first entry)
 DT
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 33.
 DE
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.
 XX
 OS Synthetic.
 XX
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX
 XX 04-AUG-2000; 2000WO-US021296.
 PF
 XX 06-AUG-1999; 99US-0147627P.
 PR
 XX 23-AUG-1999; 99US-0150315P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Dennis MS;
 XX
 XX WPI; 2001-211069/21.
 DR
 XX
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX
 XX Example 1; Fig 4; 80pp; English.
 PS
 XX This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thrombembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicaemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX

CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX
 SQ Sequence 24 AA;

Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 92.3%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
 DB 3 WEVLCWTWETCER 15

RESULT 48
 AAB90197
 ID AAB90197 standard; peptide; 24 AA.
 XX
 AC AAB90197;
 XX
 XX 23-MAY-2001 (first entry)
 DT
 XX Factor VIIa (FVIIa) antagonist peptide SEQ ID 55.
 DE
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.
 XX
 OS Synthetic.
 XX
 XX WO200110892-A2.
 PN
 XX 15-FEB-2001.
 PD
 XX
 XX 04-AUG-2000; 2000WO-US021296.
 PF
 XX 06-AUG-1999; 99US-0147627P.
 PR
 XX 23-AUG-1999; 99US-0150315P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Dennis MS;
 XX
 XX WPI; 2001-211069/21.
 DR
 XX
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic
 PT and prophylactic methods, inhibits FVII/FVIIa mediated processes and
 PT blocks initial events of blood coagulation.
 XX
 XX Example 1; Fig 4; 80pp; English.
 PS
 XX This invention relates to peptides which act as antagonist of Factor VIIa
 CC (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation
 CC factor. FVIIa antagonist peptides are useful for inhibiting FVIIa
 CC activity in the presence of a tissue factor (TF) and for treating a
 CC TF/FVIIa mediated disease or disorder in a host. Diseases which can be
 CC treated include chronic thrombembolic diseases or disorders associated
 CC with fibrin formation including vascular disorders such as deep venous
 CC thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis,
 CC arteriosclerosis and restenosis following angioplasty, acute and chronic
 CC indications such as inflammation, septic shock, septicaemia, hypotension,
 CC cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory
 CC distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC)
 CC and other diseases like inflammatory disorders. The antagonist peptides
 CC are also useful in research, and for diagnostic, therapeutic and
 CC prophylactic purposes. The present sequence represents a factor VIIa
 CC antagonist peptide of the invention
 XX

SQ Sequence 24 AA;

Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 12
 |||||
 DB 3 WEVLCWTWETCE 14

RESULT 49
 AAB90180
 ID AAB90180 standard; peptide; 24 AA.
 XX AC AAB90180;
 XX DT 23-MAY-2001 (first entry)
 XX DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 38.
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.
 XX OS Synthetic.
 XX WO200110892-A2.
 XX PD 15-FEB-2001.
 XX PF 04-AUG-2000; 2000WO-US021296.
 XX PR 06-AUG-1999; 99US-0147627P.
 XX PR 23-AUG-1999; 99US-0150315P.
 XX PA (GETH) GENENTECH INC.
 XX PI Dennis MS;
 XX WPT; 2001-211069/21.
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic and prophylactic methods, inhibits FVII/FVIIa mediated processes and blocks initial events of blood coagulation.
 XX Example 1; Fig 4; 80pp; English.

CC This invention relates to peptides which act as antagonist of Factor VIIa (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation factor. FVIIa antagonist peptides are useful for inhibiting FVIIa activity in the presence of a tissue factor (TF) and for treating a TF/FVIIa mediated disease or disorder in a host. Diseases which can be treated include chronic thrombembolic diseases or disorders associated with fibrin formation including vascular disorders such as deep venous thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis, arteriosclerosis and restenosis following angioplasty, acute and chronic indications such as inflammation, septic shock, septicaemia, hypotension, cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC) and other diseases like inflammatory disorders. The antagonist peptides are also useful in research, and for diagnostic, therapeutic and prophylactic purposes. The present sequence represents a factor VIIa antagonist peptide of the invention

SQ Sequence 24 AA;
 Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 13
 |||||
 DB 3 WEVLCWTWETCE 15

RESULT 50
 AAB90193
 ID AAB90193 standard; peptide; 24 AA.
 XX AC AAB90193;
 XX DT 23-MAY-2001 (first entry)
 XX DE Factor VIIa (FVIIa) antagonist peptide SEQ ID 51.
 XX Antagonist; factor VIIa; FVIIa; blood coagulation factor; inhibitor;
 KW chronic thrombembolic disease; fibrin formation; vascular disorder;
 KW deep vein thrombosis; arterial thrombosis; stroke; metastasis;
 KW thrombolysis; arteriosclerosis; restenosis; inflammation; septic shock;
 KW septicaemia; hypotension; angioedema; ARDS.
 XX OS Synthetic.
 XX WO200110892-A2.
 XX PD 15-FEB-2001.
 XX PF 04-AUG-2000; 2000WO-US021296.
 XX PR 06-AUG-1999; 99US-0147627P.
 XX PR 23-AUG-1999; 99US-0150315P.
 XX PA (GETH) GENENTECH INC.
 XX PI Dennis MS;
 XX WPT; 2001-211069/21.
 XX New factor VIIa antagonist peptide for research, diagnostic, therapeutic and prophylactic methods, inhibits FVII/FVIIa mediated processes and blocks initial events of blood coagulation.
 XX Example 1; Fig 4; 80pp; English.

CC This invention relates to peptides which act as antagonist of Factor VIIa (FVIIa). FVIIa is a trypsin-like serine protease blood coagulation factor. FVIIa antagonist peptides are useful for inhibiting FVIIa activity in the presence of a tissue factor (TF) and for treating a TF/FVIIa mediated disease or disorder in a host. Diseases which can be treated include chronic thrombembolic diseases or disorders associated with fibrin formation including vascular disorders such as deep venous thrombosis, arterial thrombosis, stroke, tumour metastasis, thrombolysis, arteriosclerosis and restenosis following angioplasty, acute and chronic indications such as inflammation, septic shock, septicaemia, hypotension, cardiopulmonary bypass surgery, hereditary angioedema, adult respiratory distress syndrome (ARDS), disseminated intravascular coagulopathy (DIC) and other diseases like inflammatory disorders. The antagonist peptides are also useful in research, and for diagnostic, therapeutic and prophylactic purposes. The present sequence represents a factor VIIa antagonist peptide of the invention

SQ Sequence 24 AA;
 Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 13
 |||||
 DB 3 WEVLCWTWETCE 15

Query Match 94.4%; Score 84; DB 4; Length 24;
 Best Local Similarity 92.3%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 13
 |||||
 DB 3 WEVLCWTWETCE 15

Search completed: March 28, 2006, 11:47:05

Job time : 227 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:47:25 ; Search time 38 Seconds
(without alignments)
32.916 Million cell updates/sec

Title: US-10-639-076-4

Perfect score: 89

Sequence: 1 WEVLCTWETCER 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	57.3	282	2 S70117	hypothetical prote
2	49	55.1	395	2 B96610	hypothetical prote
3	46	51.7	427	2 T41257	hypothetical prote
4	46	51.7	1080	2 T19048	probable Pro-X car
5	46	51.7	1121	2 T21303	hypothetical prote
6	46	51.7	1230	2 S47466	cellulose 1,4-beta
7	44	49.4	203	2 A53294	superoxide dismuta
8	43	48.3	516	2 T10000	cytochrome P450 (C
9	43	48.3	524	2 T09999	probable cytochrom
10	43	48.3	524	2 T09944	immunogenic protei
11	42	47.2	347	2 D69373	hypothetical prote
12	42	47.2	475	2 T45766	hypothetical prote
13	42	47.2	501	2 E85025	urease (EC 3.5.1.5
14	42	47.2	569	2 S75169	probable calcium-a
15	42	47.2	731	2 T09172	3-dehydroshikimate
16	41.5	46.6	359	2 A22421	methionine synthet
17	41.5	46.6	519	2 S16808	hypothetical prote
18	41	46.1	242	2 E71621	hypothetical prote
19	41	46.1	276	2 T47351	hypothetical prote
20	41	46.1	278	2 S48776	hypothetical prote
21	41	46.1	306	2 A75316	hypothetical prote
22	41	46.1	330	2 S08500	QUTG protein - Eme
23	41	46.1	340	2 B31277	hypothetical prote
24	41	46.1	481	2 T10036	hypothetical prote
25	41	46.1	494	2 T16858	hypothetical prote
26	41	46.1	575	2 A96766	unknown protein F2
27	41	46.1	594	2 D71347	conserved hypothet
28	41	46.1	732	2 AD0014	primosomal protein
29	41	46.1	856	2 G96814	hypothetical prote

30	41	46.1	951	2 T00260	hypothetical prote
31	41	46.1	1085	2 H82511	hypothetical prote
32	41	46.1	1711	2 T21432	hypothetical prote
33	40.5	45.5	1256	2 T47325	hypothetical prote
34	40.5	45.5	4861	2 S71752	giant protein p619
35	40	44.9	280	2 A70513	hypothetical prote
36	40	44.9	295	2 S46749	hypothetical prote
37	40	44.9	306	2 D87531	glycosyl transfera
38	40	44.9	415	2 T49840	hypothetical prote
39	40	44.9	416	2 G82232	cysteine proteinas
40	40	44.9	614	2 T19963	enhancer of split
41	40	44.9	741	2 B49555	hypothetical prote
42	40	44.9	855	2 T29775	dehydroshikimate d
43	39.5	44.4	348	2 JN0250	hypothetical prote
44	39.5	44.4	551	2 D75195	hypothetical prote
45	39	43.8	93	2 AC3330	hypothetical trans
46	39	43.8	286	2 C95847	transporter, dme f
47	39	43.8	301	2 AE3273	cyclin protein-like
48	39	43.8	317	2 T49995	galactoside transp
49	39	43.8	333	2 AC3597	G protein-coupled
50	39	43.8	340	2 JC7695	hypothetical prote
51	39	43.8	361	2 T20105	patatin-like prote
52	39	43.8	428	2 F85437	conserved hypothet
53	39	43.8	429	2 B87039	hexuronate transpo
54	39	43.8	438	2 H87371	hypothetical prote
55	39	43.8	438	2 D70528	hypothetical prote
56	39	43.8	471	2 T15394	hypothetical prote
57	39	43.8	472	2 T41684	probable sterol O
58	39	43.8	479	2 D86340	protein F2D10.30 [
59	39	43.8	509	2 H90994	hypothetical prote
60	39	43.8	509	2 E85840	hypothetical prote
61	39	43.8	519	2 T45764	hypothetical prote
62	39	43.8	581	2 H69452	hypothetical prote
63	39	43.8	779	2 AG1978	hypothetical prote
64	39	43.8	993	2 A36873	protein-tyrosine k
65	39	43.8	1253	2 T46248	hypothetical prote
66	39	43.8	1253	2 T14349	Shyc protein - mou
67	39	43.8	1305	2 T00670	probable inositol
68	39	43.8	1607	2 T43212	insulin-like growt
69	39	43.8	1829	2 T34239	hypothetical prote
70	39	43.8	2049	2 T29227	hypothetical prote
71	38.5	43.3	1011	2 T45718	receptor-kinase li
72	38.5	43.3	1737	2 T00209	MEG8 protein - hu
73	38	42.7	104	2 C75046	hypothetical prote
74	38	42.7	111	2 T14306	glycine-rich prote
75	38	42.7	117	2 T49511	hypothetical prote
76	38	42.7	179	2 T02878	probable resistanc
77	38	42.7	179	2 T02915	probable disease r
78	38	42.7	179	2 T02890	probable disease r
79	38	42.7	214	1 ASLJG5	vif protein - simi
80	38	42.7	214	1 ASLJSM	vif protein - simi
81	38	42.7	214	2 S07989	vif protein - simi
82	38	42.7	214	2 T11561	vif protein - simi
83	38	42.7	215	1 ASLJGW	vif protein - huma
84	38	42.7	215	1 ASLJGG	vif protein - huma
85	38	42.7	215	1 ASLJS2	vif protein - huma
86	38	42.7	215	1 ASLJSW	vif protein - huma
87	38	42.7	215	2 S53093	vif protein - huma
88	38	42.7	215	2 S12154	vif protein - huma
89	38	42.7	215	2 A86437	F28K20.7 protein -
90	38	42.7	216	2 S08437	vif protein - huma
91	38	42.7	229	1 C45345	vif protein - capr
92	38	42.7	244	2 A75418	phosphoesterase-re
93	38	42.7	262	2 C84800	3-oxo-5-alpha-ster
94	38	42.7	262	2 T22371	hypothetical prote
95	38	42.7	267	2 G84004	spore outer layer
96	38	42.7	292	2 T45680	hypothetical prote
97	38	42.7	301	2 T29667	hypothetical prote
98	38	42.7	323	1 A28396	prostaglandin-F sy
99	38	42.7	323	1 JH0575	prostaglandin-F sy
100	38	42.7	323	2 B57407	3alpha-hydroxyster
101	38	42.7	323	2 I73674	chloroacetic reduct
102	38	42.7	330	2 E84479	En/Spm-like transp

103	38	42.7	451	2	T33233	hypothetical prote	176	37	41.6	629	2	C82598	glucose inhibited
104	38	42.7	454	2	T21358	hypothetical prote	177	37	41.6	642	2	C96777	F25A4.24 [imported
105	38	42.7	468	2	I64182	Na+/H-exchanging	178	37	41.6	674	2	F82844	oligopeptidase A x
106	38	42.7	471	1	S62590	peptidyl-prolyl ci	179	37	41.6	699	2	A43734	probable protein k
107	38	42.7	480	2	C70802	hypothetical prote	180	37	41.6	751	2	T04430	hypothetical prote
108	38	42.7	487	2	T32341	hypothetical prote	181	37	41.6	881	2	A97107	alanyl-tRNA synthe
109	38	42.7	519	2	G84707	probable MYB fam1	182	37	41.6	925	2	T18747	ksr protein - frui
110	38	42.7	525	2	T21357	hypothetical prote	183	37	41.6	1003	2	T13856	protein ZK742.1 li
111	38	42.7	532	2	T27235	hypothetical prote	184	37	41.6	1140	1	G89113	M polyprotein prec
112	38	42.7	539	2	S53529	monophenol monooxy	185	37	41.6	1148	1	JQ1604	tegument protein 0
113	38	42.7	539	2	Af2456	hypothetical prote	186	37	41.6	1319	2	S55598	phosphoribosylform
114	38	42.7	565	2	T47330	hypothetical prote	187	37	41.6	1322	2	D82685	insulin-like growt
115	38	42.7	585	2	S44851	K12H4.7 protein -	188	37	41.6	1363	2	T43220	hypothetical prote
116	38	42.7	649	2	S28588	outD protein - Erw	189	36.5	41.0	205	2	T14745	octopamine recepto
117	38	42.7	660	2	E81839	probable transmemb	190	36.5	41.0	601	2	JH0170	tyramine receptor
118	38	42.7	661	2	T47467	hypothetical prote	191	36.5	41.0	601	2	S12004	hypothetical prote
119	38	42.7	669	2	D64137	betT protein homol	192	36.5	41.0	1171	2	T12956	P-glycoprotein ppg
120	38	42.7	675	2	E81101	transporter, BCC7	193	36.5	41.0	1286	2	A42150	depressant insect
121	38	42.7	759	2	G64979	hypothetical prote	194	36	40.4	61	2	B34123	depressant insect
122	38	42.7	807	1	WNA9D15	late 100K protein	195	36	40.4	61	2	C59352	depressant insect
123	38	42.7	851	2	T38497	hypothetical prote	196	36	40.4	85	2	A61616	conserved hypothet
124	38	42.7	881	2	G96574	hypothetical prote	197	36	40.4	97	2	AF3035	hypothetical prote
125	38	42.7	892	2	S57055	probable membrane	198	36	40.4	99	2	E98250	probable IS1560 tr
126	38	42.7	915	2	A49874	metabotropic gluta	199	36	40.4	112	2	G70624	hypothetical prote
127	38	42.7	1017	2	S67804	LRG1 protein - yea	200	36	40.4	140	2	G90038	conserved hypothet
128	38	42.7	1052	2	B49120	hypothetical prote	201	36	40.4	158	2	AE3053	hypothetical prote
129	38	42.7	1063	2	T46284	protein-tyrosine k	202	36	40.4	158	2	H98232	conserved hypothet
130	38	42.7	1520	1	TVFFFA	hypothetical prote	203	36	40.4	161	2	AE0357	proline/betaine tr
131	37.5	42.1	229	2	A69762	hypothetical prote	204	36	40.4	170	2	B97811	C-reactive protein
132	37.5	42.1	317	2	T51204	hypothetical prote	205	36	40.4	200	2	S62762	C-reactive protein
133	37.5	42.1	619	2	T27026	hypothetical prote	206	36	40.4	218	2	C25193	C-reactive protein
134	37.5	42.1	934	1	A34372	complement C6 prec	207	36	40.4	218	2	B25193	ABC transporter (A
135	37	41.6	85	2	A40472	depressant insect	208	36	40.4	231	2	B69756	C-reactive protein
136	37	41.6	154	2	A13020	conserved hypothet	209	36	40.4	242	2	B25192	C-reactive protein
137	37	41.6	154	2	H98263	hypothetical prote	210	36	40.4	242	2	A25192	C-reactive protein
138	37	41.6	188	2	S61516	dihydrodiol dehydr	211	36	40.4	263	1	EQBOA	enkephalin e-12 pr
139	37	41.6	213	2	T01464	hypothetical prote	212	36	40.4	282	2	AI0948	hypothetical prote
140	37	41.6	243	2	B84490	En/Spm-like transp	213	36	40.4	284	2	A70976	hypothetical prote
141	37	41.6	244	2	S25988	hypothetical prote	214	36	40.4	289	2	T44462	DNA-binding protei
142	37	41.6	252	2	S61515	dihydrodiol dehydr	215	36	40.4	296	2	T35477	probable oxidoredu
143	37	41.6	258	2	B84455	En/Spm-like transp	216	36	40.4	302	2	AD0709	conserved hypothet
144	37	41.6	295	2	G90934	probable excinucle	217	36	40.4	316	2	T50027	annexin-like prote
145	37	41.6	295	2	C85783	hypothetical prote	218	36	40.4	323	1	JC2330	luteal 20-alpha-hy
146	37	41.6	295	2	E64933	hypothetical prote	219	36	40.4	324	2	F44221	orf5 protein - Aut
147	37	41.6	308	2	AE2359	hypothetical prote	220	36	40.4	324	2	D91277	probable transmemb
148	37	41.6	318	2	AI2236	hypothetical prote	221	36	40.4	324	2	D91277	probable transmemb
149	37	41.6	320	2	I73675	chlorocone reduct	222	36	40.4	324	2	D86118	hypothetical 35.5K
150	37	41.6	323	2	A53436	3-alpha-hydroxyste	223	36	40.4	324	2	S56435	hypothetical prote
151	37	41.6	323	2	I73676	chlorocone reduct	224	36	40.4	334	2	C86813	aldose 1-epimerase
152	37	41.6	323	2	JC5240	3alpha-hydroxychol	225	36	40.4	345	2	T19676	hypothetical prote
153	37	41.6	329	2	I53872	dihydrodiol dehydr	226	36	40.4	353	2	G84515	hypothetical prote
154	37	41.6	357	2	T34012	hypothetical prote	227	36	40.4	362	2	T32669	histone deacetylase
155	37	41.6	371	2	B83900	gentisate 1,2-diox	228	36	40.4	374	2	G90100	pentaxin PTX3 prec
156	37	41.6	381	2	G75589	hypothetical prote	229	36	40.4	381	2	A44323	flagellar biosynth
157	37	41.6	382	2	H64950	flagellar biosynth	230	36	40.4	383	2	C84958	ecdysone-inducible
158	37	41.6	382	2	B85801	hypothetical prote	231	36	40.4	390	1	B49070	sugar-binding prot
159	37	41.6	382	2	F90952	flagellar biosynth	232	36	40.4	412	2	F89796	hypothetical prote
160	37	41.6	383	2	AF0745	flagellar biosynth	233	36	40.4	422	2	T48680	hypothetical prote
161	37	41.6	383	2	A55546	chemoattractant re	234	36	40.4	427	2	A55496	apexin precursor -
162	37	41.6	392	2	A12138	histone deacetylase	235	36	40.4	432	2	T10894	D-xylose proton-sy
163	37	41.6	424	2	JC7102	histone deacetylase	236	36	40.4	433	2	G86812	glycosyl hydrolase
164	37	41.6	428	2	JC5834	histone deacetylase	237	36	40.4	453	2	T39155	integral membrane
165	37	41.6	443	2	A54813	CAMP receptor CAR4	238	36	40.4	471	2	A41680	hypothetical prote
166	37	41.6	461	2	T20163	hypothetical prote	239	36	40.4	475	2	T20165	hypothetical prote
167	37	41.6	480	1	S60381	RPD3 protein homol	240	36	40.4	487	2	T45923	hypothetical prote
168	37	41.6	490	2	A46391	CAMP receptor subt	241	36	40.4	495	2	C95144	glucose-6-phosphat
169	37	41.6	518	2	T50745	phytoene dehydroge	242	36	40.4	495	2	A98012	glucose-6-phosphat
170	37	41.6	526	2	JC4533	cytochrome P450 4F	243	36	40.4	500	2	S22458	cellulase (EC 3.2.
171	37	41.6	558	2	T40651	pre-mrna splicing	244	36	40.4	503	2	E70602	probable membranep
172	37	41.6	567	2	T16105	hypothetical prote	245	36	40.4	537	2	A86154	hypothetical prote
173	37	41.6	569	2	T22928	hypothetical prote	246	36	40.4	540	2	B47417	insulin receptor-r
174	37	41.6	582	2	T16104	hypothetical prote	247	36	40.4	554	2	T40234	phosphoglucomutase
175	37	41.6	609	2	T52524	hypothetical prote	248	36	40.4				

249	36	40.4	575	2	A47214	Jk-recombination s	322	35	39.3	258	2	A10764	cyclase hisf [impo
250	36	40.4	605	2	JC5673	receptor tyrosine	323	35	39.3	259	2	A87623	PAP2 homolog prote
251	36	40.4	610	2	I48612	developmental kina	324	35	39.3	260	2	C83537	hypothetical prote
252	36	40.4	614	2	A45053	membrane protein E	325	35	39.3	266	2	S40988	hypothetical prote
253	36	40.4	626	2	I48614	developmental kina	326	35	39.3	274	2	T48428	hypothetical prote
254	36	40.4	627	2	B64710	site-specific DNA-	327	35	39.3	280	2	S72844	beta-aspartate met
255	36	40.4	680	2	T45736	hypothetical prote	328	35	39.3	281	2	C87073	conserved hypotet
256	36	40.4	694	2	C83826	penicillin-binding	329	35	39.3	286	2	T38888	probable oxidoredu
257	36	40.4	697	2	T16306	hypothetical prote	330	35	39.3	293	2	T31146	probable DNA inver
258	36	40.4	708	2	T51026	hypothetical prote	331	35	39.3	298	2	T20044	hypothetical prote
259	36	40.4	713	2	S76766	hypothetical prote	332	35	39.3	302	2	T19348	B cell-associated
260	36	40.4	826	1	A31822	villin - chicken	333	35	39.3	305	2	A46476	hypothetical prote
261	36	40.4	837	2	I64236	valine-tRNA ligase	334	35	39.3	305	2	C83743	hypothetical prote
262	36	40.4	864	2	A49070	ecdysone-inducible	335	35	39.3	312	2	B96512	hypothetical prote
263	36	40.4	879	2	A55881	beta-mannosidase (336	35	39.3	314	2	T21926	2alpha-hydroxyste
264	36	40.4	927	2	A45039	CRF4 protein - yea	337	35	39.3	323	1	A45366	hypothetical prote
265	36	40.4	938	2	S20480	trag protein - Esc	338	35	39.3	323	2	H90434	hypothetical prote
266	36	40.4	968	2	T29466	hypothetical prote	339	35	39.3	324	1	JC4280	carboxyl reductase
267	36	40.4	982	1	VLJUVS	env polypeptide pr	340	35	39.3	326	1	S15835	3-oxo-5beta-steroi
268	36	40.4	983	1	E45390	env polypeptide pr	341	35	39.3	326	1	S41120	cholestenone 5beta
269	36	40.4	992	2	A39931	protein-tyrosine k	342	35	39.3	329	2	A48805	insulin-like growt
270	36	40.4	998	2	I58351	receptor protein-t	343	35	39.3	333	2	D83585	hypothetical prote
271	36	40.4	1000	2	JC5672	receptor tyrosine	344	35	39.3	345	2	T32203	hypothetical prote
272	36	40.4	1011	2	S18827	Fit3 protein - mou	345	35	39.3	359	2	T46160	caifeic acid O-met
273	36	40.4	1056	2	AD0447	probable insectici	346	35	39.3	380	2	S53293	SCS3 protein - yea
274	36	40.4	1056	2	B96748	hypothetical prote	347	35	39.3	390	2	A87274	hypothetical prote
275	36	40.4	1146	2	B35962	protein-tyrosine k	348	35	39.3	391	2	T35574	probable alanine r
276	36	40.4	1178	2	S30431	MSP-300 protein -	349	35	39.3	393	2	AD2219	hypothetical prote
277	36	40.4	1182	2	A35962	protein-tyrosine k	350	35	39.3	395	2	S47987	actin-related prot
278	36	40.4	1182	2	T48378	hairless protein -	351	35	39.3	404	2	T19831	hypothetical prote
279	36	40.4	1196	2	T23832	protein-tyrosine k	352	35	39.3	417	2	C86603	muramoyltalanine-gl
280	36	40.4	1268	2	B36502	insulin receptor-r	353	35	39.3	417	2	H72021	UDP-N-acetylmutamo
281	36	40.4	1300	2	A36502	insulin receptor-r	354	35	39.3	420	2	E75130	hypothetical prote
282	36	40.4	1810	2	E88481	protein C16A3.2 (i	355	35	39.3	422	2	A56640	CDC4 repeat unit-c
283	36	40.4	2911	2	T20566	hypothetical prote	356	35	39.3	426	2	T05676	hypothetical prote
284	36	40.4	3144	2	S64791	VPS13 protein - ye	357	35	39.3	430	2	S62500	actin-related prot
285	35.5	39.9	147	2	T49670	hypothetical prote	358	35	39.3	451	1	JC6180	stearyl-CoA 9-des
286	35.5	39.9	256	2	H36857	B26R protein - var	359	35	39.3	457	2	T51528	hypothetical prote
287	35.5	39.9	395	2	T32309	hypothetical prote	360	35	39.3	484	2	C82171	cardiolipin syntha
288	35.5	39.9	567	2	A71463	probable sulfate t	361	35	39.3	489	2	D82325	cytoplasmic axial
289	35.5	39.9	600	2	S07638	spore coat protein	362	35	39.3	491	2	JE0276	voltage-gated pota
290	35.5	39.9	716	2	T51354	cyclic nucleotide-	363	35	39.3	494	2	T28660	probable adhesin P
291	35.5	39.9	731	2	B86132	hypothetical prote	364	35	39.3	507	2	T27627	hypothetical prote
292	35.5	39.9	735	2	G91290	hypothetical prote	365	35	39.3	520	2	T14312	hypothetical prote
293	35.5	39.9	771	2	AF2381	hypothetical prote	366	35	39.3	528	2	D86456	hypothetical prote
294	35.5	39.9	796	1	JC1285	protein-tyrosine-p	367	35	39.3	532	2	H85035	probable protein k
295	35.5	39.9	802	1	A36065	protein-tyrosine-p	368	35	39.3	547	1	S28904	hypothetical prote
296	35.5	39.9	829	1	A47373	probable complemen	369	35	39.3	582	2	F84807	intercellular adhe
297	35.5	39.9	1053	2	S46199	probable membrane	370	35	39.3	586	2	T03684	hypothetical prote
298	35.5	39.9	1140	2	AE0180	hypothetical prote	371	35	39.3	587	2	AG3169	phosphoprotein pho
299	35.5	39.9	1897	2	T28621	hypothetical prote	372	35	39.3	607	2	A36792	conserved hypotet
300	35	39.3	34	2	G82415	hypothetical prote	373	35	39.3	697	2	A26132	hypothetical prote
301	35	39.3	86	2	S23992	trbE protein - Esc	374	35	39.3	714	2	E83516	gag-abl pol polypr
302	35	39.3	99	2	AH2305	hypothetical prote	375	35	39.3	753	2	T05649	hypothetical prote
303	35	39.3	109	2	S76789	glutaredoxin - Syn	376	35	39.3	757	2	F87304	beta-N-acetylhexos
304	35	39.3	124	1	T18HB	trypsin inhibitor	377	35	39.3	779	2	D82995	conserved hypotet
305	35	39.3	132	2	G97283	ribosomal protein	378	35	39.3	790	2	A36827	protein-tyrosine k
306	35	39.3	133	2	AC2331	30S ribosomal prot	379	35	39.3	829	2	A40894	RNA-directed RNA p
307	35	39.3	142	2	I51651	midline homolog -	380	35	39.3	832	2	A40205	Na+/H+-exchanging
308	35	39.3	142	2	JC4168	midline precursor	381	35	39.3	843	2	T25742	hypothetical prote
309	35	39.3	142	2	JC4272	pleiotrophic facto	382	35	39.3	885	2	B86257	NBS/LRR disease re
310	35	39.3	142	2	JC4273	pleiotrophic facto	383	35	39.3	919	2	T37062	probable transcrip
311	35	39.3	155	2	AD2392	transcription regu	384	35	39.3	920	2	T02953	aspartate kinase (
312	35	39.3	184	2	AG0737	probable membrane	385	35	39.3	981	1	FOVWGM	gag-abl polyprotei
313	35	39.3	185	2	C96808	protein F28K19.4 (386	35	39.3	1023	2	T30257	IgG Fc binding pro
314	35	39.3	192	2	T26544	hypothetical prote	387	35	39.3	1123	2	A39962	kinase-related tra
315	35	39.3	198	2	AF1870	hypothetical prote	388	35	39.3	1130	1	TVHUA	protein-tyrosine k
316	35	39.3	225	1	CYFGE	epsilonon-crystallin	389	35	39.3	1201	2	T00444	hypothetical prote
317	35	39.3	229	2	T30734	hypothetical prote	390	35	39.3	1266	2	A12195	two-component hybr
318	35	39.3	238	2	T34710	hypothetical prote	391	35	39.3	1367	1	IGHUR1	insulin-like growt
319	35	39.3	240	2	T19349	hypothetical prote	392	35	39.3	1371	2	A33837	insulin-like growt
320	35	39.3	252	2	B69641	cyclase hisf - Bac	393	35	39.3	1402	2	S62557	probable calcium-t
321	35	39.3	258	1	OVBHF	cyclase hisf - Sal	394	35	39.3	1444	2	T18856	angiogenesis inhib

395	35	39.3	1920	2	T13893	gene hindsight pro	468	34	38.2	258	2	B90982	imidazoleglycerol-
396	35	39.3	2352	2	T34331	alpha-glucan synth	469	34	38.2	258	2	H85827	imidazoleglycerol-
397	34.5	38.8	274	2	T39166	inorganic phosphat	470	34	38.2	258	2	B54052	cyclase hisF - kle
398	34.5	38.8	391	2	T29277	hypothetical prote	471	34	38.2	259	2	A65070	hypothetical prote
399	34.5	38.8	417	2	C72032	ct573 hypothetical	472	34	38.2	259	2	B91096	probable lipoprote
400	34.5	38.8	417	2	D86592	CT573 hypothetical	473	34	38.2	261	2	S68234	Lasp-1 protein - h
401	34.5	38.8	417	2	A81509	conserved hypothet	474	34	38.2	264	2	H83224	phosphonate transp
402	34.5	38.8	419	2	S72325	glucan 1,3-beta-gl	475	34	38.2	270	2	AD1408	hypothetical prote
403	34.5	38.8	461	2	AF1179	hexose phosphate t	476	34	38.2	270	2	AD1784	hypothetical prote
404	34.5	38.8	544	2	AB0716	probable substrate	477	34	38.2	272	2	E64694	probable lipoprote
405	34.5	38.8	562	2	A65166	hypothetical 63.2K	478	34	38.2	272	2	T35624	hypothetical prote
406	34.5	38.8	562	2	B91194	probable enzyme [i	479	34	38.2	289	2	T22834	hypothetical prote
407	34.5	38.8	562	2	C86041	probable enzyme yi	480	34	38.2	299	2	T18563	hypothetical prote
408	34.5	38.8	572	2	T50404	probable inorganic	481	34	38.2	301	2	A70787	hypothetical homoc
409	34.5	38.8	572	2	S72249	trithorax protein	482	34	38.2	308	2	T38947	hypothetical prote
410	34.5	38.8	692	2	H70362	glycogen phosphory	483	34	38.2	309	1	S34198	IGF Fc receptor II
411	34.5	38.8	832	2	JC8051	protein tyrosine p	484	34	38.2	318	2	S37648	hypothetical prote
412	34.5	38.8	837	2	A21112	mucin-like peptide	485	34	38.2	319	2	S73159	hypothetical prote
413	34.5	38.8	1220	2	A56136	jagged protein pre	486	34	38.2	321	2	AB1054	probable membrane
414	34.5	38.8	3020	2	A43932	mucin 2 precursor,	487	34	38.2	322	1	A39350	3alpha-hydroxyster
415	34	38.2	54	2	E85745	unknown protein en	488	34	38.2	323	1	A56424	estradiol 17beta-d
416	34	38.2	69	2	C90495	hypothetical prote	489	34	38.2	328	2	C72370	tryptophan-tRNA li
417	34	38.2	83	2	H81084	hypothetical prote	490	34	38.2	329	2	T47870	hypothetical prote
418	34	38.2	94	2	T38652	hypothetical prote	491	34	38.2	331	1	LNM58R	IGF Fc receptor, I
419	34	38.2	103	2	A24114	glutaredoxin limpo	492	34	38.2	333	2	S36714	alpha-tubulin supp
420	34	38.2	105	2	E82613	hypothetical prote	493	34	38.2	344	2	AD0944	L-rhamnose-proton
421	34	38.2	114	2	A83300	hypothetical prote	494	34	38.2	344	2	A42436	L-rhamnose-H+ tran
422	34	38.2	118	2	T11584	hypothetical prote	495	34	38.2	344	2	AH0041	L-rhamnose-hypoth
423	34	38.2	120	2	E95343	hypothetical prote	496	34	38.2	355	2	E75577	conserved hypotet
424	34	38.2	121	2	S28799	hypothetical prote	497	34	38.2	365	2	S55498	alpha(1,3/4)-fucos
425	34	38.2	122	2	JQ0150	hypothetical 13K p	498	34	38.2	372	2	S23936	L-selectin precurs
426	34	38.2	127	2	S37901	hypothetical prote	499	34	38.2	372	2	A53050	brefeldin A estera
427	34	38.2	132	1	R3KT8	ribosomal protein	500	34	38.2	373	2	T10577	hypothetical prote
428	34	38.2	132	2	S78262	ribosomal protein	501	34	38.2	374	2	F96525	protein rin1.23 [
429	34	38.2	132	2	T07521	ribosomal protein	502	34	38.2	375	2	F69551	coenzyme PQQ synth
430	34	38.2	136	1	R3R28	ribosomal protein	503	34	38.2	375	2	S58784	probable membrane
431	34	38.2	136	1	R3ZMB	ribosomal protein	504	34	38.2	379	2	JC6178	serotonin receptor
432	34	38.2	146	2	T28641	Y4JN protein - Rni	505	34	38.2	394	2	T08757	probable translati
433	34	38.2	164	2	T44054	glycoprotein gp82/	506	34	38.2	396	2	T19272	hypothetical prote
434	34	38.2	167	2	T35320	probable membrane	507	34	38.2	401	2	T31915	hypothetical prote
435	34	38.2	184	2	F90873	probable antitermi	508	34	38.2	417	2	T20327	hypothetical prote
436	34	38.2	184	2	A90903	probable ante-term	509	34	38.2	420	2	S73475	serine-tRNA ligase
437	34	38.2	184	2	AB3163	IS 426 transposase	510	34	38.2	420	2	A84492	probable PttA-like
438	34	38.2	185	2	F70986	probable integral	511	34	38.2	428	2	A55044	hypothetical prote
439	34	38.2	187	2	A93478	acid tolerance reg	512	34	38.2	438	2	T12835	beta-4C-adrenergic
440	34	38.2	188	2	H85713	unknown protein en	513	34	38.2	451	2	A97182	hypothetical prote
441	34	38.2	191	2	D70033	conserved hypotet	514	34	38.2	451	2	H84479	acyl-CoA reductase
442	34	38.2	193	2	S39829	probable membrane	515	34	38.2	451	2	T31708	probable PttA-like
443	34	38.2	195	2	AC2583	two component resp	516	34	38.2	453	2	T50645	hypothetical prote
444	34	38.2	195	2	A97365	actr protein (AF22	517	34	38.2	453	2	T15374	glucan endo-1,3-be
445	34	38.2	199	2	S73702	hypothetical prote	518	34	38.2	455	2	A55050	hypothetical prote
446	34	38.2	210	2	D75025	probable phosphos	519	34	38.2	460	2	H70924	enigma - human
447	34	38.2	212	2	PQ0518	envelope protein -	520	34	38.2	461	2	G90642	hypothetical prote
448	34	38.2	215	2	B91027	probable S-transfe	521	34	38.2	461	2	G85493	hypothetical prote
449	34	38.2	215	2	C85871	probable S-transfe	522	34	38.2	461	2	C64733	protein transport
450	34	38.2	215	2	D65002	hypothetical prote	523	34	38.2	464	2	C75470	isocitrate lyase -
451	34	38.2	215	2	S34163	homeotic protein H	524	34	38.2	464	2	T28936	glutamate decarbox
452	34	38.2	216	2	AB1052	probable hexulose-	525	34	38.2	476	2	S75150	hypothetical prote
453	34	38.2	216	2	S56421	Probable hexulose-	526	34	38.2	478	2	A86142	hypothetical prote
454	34	38.2	216	2	D91275	Probable hexulose-	527	34	38.2	481	2	E86356	protein T25K16.17
455	34	38.2	216	2	D86116	Probable hexulose-	528	34	38.2	484	2	S58868	G protein-coupled
456	34	38.2	222	2	A31685	BFI protein - fowl	529	34	38.2	500	2	A52032	glycerol kinase [i
457	34	38.2	222	2	F85941	hypothetical prote	530	34	38.2	503	2	S31126	hypothetical prote
458	34	38.2	223	2	S75380	probable lipoprote	531	34	38.2	503	2	E82730	peptide synthase x
459	34	38.2	235	2	A54951	tissue factor path	532	34	38.2	504	2	C85485	probable carnitine
460	34	38.2	240	2	B43909	myogenic protein M	533	34	38.2	504	2	C90634	probable carnitine
461	34	38.2	242	2	A42668	myogenic factor MR	534	34	38.2	504	2	H64724	probable carnitine
462	34	38.2	242	2	S12385	myf-6 protein - hu	535	34	38.2	505	2	A00511	probable carnitine
463	34	38.2	242	2	A34872	muscle-specific re	536	34	38.2	506	2	B87102	conserved membrane
464	34	38.2	242	2	JC1233	muscle-specific re	537	34	38.2	506	2	H70928	hypothetical prote
465	34	38.2	242	2	A40571	testis-specific pr	538	34	38.2	508	2	D71408	hypothetical prote
466	34	38.2	255	2	A40571	testis-specific pr	539	34	38.2	523	2	S42727	translation initia
467	34	38.2	258	1	OYECHF	imidazoleglycerol-	540	34	38.2	523	2	T22728	hypothetical prote

541	34	38.2	524	2	S71961	translation initia	614	34	38.2	1383	2	A36080	insulin receptor p
542	34	38.2	539	2	AF2065	hypothetical prote	615	34	38.2	1594	2	F96573	protein F12W16.25
543	34	38.2	540	2	G50068	choline transporte	616	34	38.2	1846	2	T42047	insulin receptor h
544	34	38.2	540	2	B82219	transporter, BCC7	617	34	38.2	1864	1	JQ1857	genome polyprotein
545	34	38.2	541	2	D82302	iron(III) ABC tran	618	34	38.2	1866	1	GNWE2C	genome polyprotein
546	34	38.2	542	2	A55146	guanine nucleotide	619	34	38.2	1925	2	T08166	probable membrane
547	34	38.2	544	2	JC4798	seizure-related me	620	34	38.2	2029	1	TDFPLK	protein-tyrosine-p
548	34	38.2	546	2	A48026	sterol O-acyltrans	621	34	38.2	3414	1	GNWNE	genome polyprotein
549	34	38.2	550	2	T37579	DiGeorge syndrome	622	34	38.2	5825	2	T12117	polyprotein - fava
550	34	38.2	550	2	H96762	hypothetical prote	623	34	38.2	10797	2	T30192	probable peptide s
551	34	38.2	555	2	H93037	urease alpha subun	624	33.5	37.6	30	2	I77411	renin-2 - mouse (f
552	34	38.2	566	2	T25162	Frizzled-1 protein	625	33.5	37.6	112	2	B71211	hypothetical prote
553	34	38.2	568	2	J35291	urease (EC 3.5.1.5	626	33.5	37.6	147	2	S73443	hypothetical prote
554	34	38.2	569	1	URKCBP	urease (EC 3.5.1.5	627	33.5	37.6	199	2	T02787	probable submergen
555	34	38.2	569	2	C36950	urease (EC 3.5.1.5	628	33.5	37.6	210	2	A81826	transcriptional regu
556	34	38.2	571	2	F83681	urease alpha subun	629	33.5	37.6	210	2	G81049	transcriptional r
557	34	38.2	578	2	T35264	probable BCC7 fami	630	33.5	37.6	216	2	S61416	dihydrokaempferol
558	34	38.2	579	2	F70000	two-component sens	631	33.5	37.6	221	2	T22771	hypothetical prote
559	34	38.2	593	2	S51956	probable membrane	632	33.5	37.6	235	2	T24882	hypothetical prote
560	34	38.2	598	2	I51368	gamma-aminobutyric	633	33.5	37.6	256	2	T25913	hypothetical prote
561	34	38.2	598	2	F46027	gamma-aminobutyric	634	33.5	37.6	285	2	AB0782	probable esterase
562	34	38.2	599	1	ACRTGT	gamma-aminobutyric	635	33.5	37.6	354	2	G86276	hypothetical prote
563	34	38.2	599	2	S11073	gamma-aminobutyric	636	33.5	37.6	358	2	AD2878	iron-chelator util
564	34	38.2	616	2	T44237	UI00 [imported] -	637	33.5	37.6	358	2	F97654	mxcB protein (AF29
565	34	38.2	625	2	S35317	hematopoietic grow	638	33.5	37.6	358	2	S62742	endopolygalacturon
566	34	38.2	626	2	S37622	prote-oncogene - m	639	33.5	37.6	380	2	S62743	endopolygalacturon
567	34	38.2	628	1	A40802	protein-tyrosine k	640	33.5	37.6	380	2	S62743	hypothetical prote
568	34	38.2	628	1	A56707	protein-tyrosine k	641	33.5	37.6	462	2	B88613	hypothetical prote
569	34	38.2	628	2	I48781	protein-tyrosine k	642	33.5	37.6	473	2	S38065	hypothetical prote
570	34	38.2	634	2	JC7808	delta-glutamata re	643	33.5	37.6	488	2	A69344	phosphate transport
571	34	38.2	635	1	A53596	protein-tyrosine k	644	33.5	37.6	513	2	S65574	sulfate transporte
572	34	38.2	637	2	T08530	tag protein - Ent	645	33.5	37.6	565	2	C86617	sulfate transporte
573	34	38.2	637	2	S22992	tag protein - Esc	646	33.5	37.6	565	2	D72006	sphingosine-1-phos
574	34	38.2	637	2	F82218	conserved hypothet	647	33.5	37.6	568	2	JC5923	hypothetical prote
575	34	38.2	648	2	B40727	S-M checkpoint con	648	33.5	37.6	576	2	T25375	hypothetical prote
576	34	38.2	653	2	A83154	probable choline t	649	33.5	37.6	734	2	T52535	suppressor of A-ki
577	34	38.2	693	2	A10996	4-alpha-glucanotra	650	33.5	37.6	766	2	T11650	sak1 protein - fis
578	34	38.2	698	2	R84547	hypothetical prote	651	33.5	37.6	915	2	S24577	ovarian protein -
579	34	38.2	700	2	T41401	spore outgrowth fa	652	33.5	37.6	1026	2	T39612	hypothetical prote
580	34	38.2	704	2	B84685	hypothetical prote	653	33.5	37.6	1372	2	T25933	hypothetical prote
581	34	38.2	707	2	T36652	H+/K+-exchanging A	654	33.5	37.6	1477	2	T13797	tumor supressor pr
582	34	38.2	714	2	S46811	hypothetical prote	655	33.5	37.6	1513	2	A54895	mucin 2, intestina
583	34	38.2	716	2	AB1070	probable carbon st	656	33	37.1	40	2	C39560	myotoxin a 5 - pra
584	34	38.2	721	2	A98293	probable carbon st	657	33	37.1	42	1	CXRSMT	crotonamine - tropic
585	34	38.2	721	2	D86134	carbon starvation	658	33	37.1	42	1	MXRSMV	myotoxin a 6 - pra
586	34	38.2	721	2	S56580	carbon starvation	659	33	37.1	43	1	CXRSCB	toxic peptide C -
587	34	38.2	725	2	E96592	hypothetical prote	660	33	37.1	43	2	A29089	myotoxin I - midg
588	34	38.2	732	1	S05238	peptidyl-dipectida	661	33	37.1	43	2	B29089	myotoxin II - midg
589	34	38.2	733	2	E82525	primosomal protein	662	33	37.1	45	2	A37909	myotoxin - eastern
590	34	38.2	825	2	AC0039	glycerol-3-phospha	663	33	37.1	45	2	S12909	myotoxin - western
591	34	38.2	838	2	A96699	probable urease FI	664	33	37.1	51	2	D35947	crotonamine 4 precu
592	34	38.2	840	1	URJB	urease (EC 3.5.1.5	665	33	37.1	55	2	T01910	hypothetical prote
593	34	38.2	844	2	T52336	formin-binding pro	666	33	37.1	56	2	E81566	hypothetical prote
594	34	38.2	849	2	H84546	hypothetical prote	667	33	37.1	65	2	JC5324	myotoxin a precurs
595	34	38.2	902	2	E90270	conserved hypothet	668	33	37.1	86	2	S25643	hypothetical prote
596	34	38.2	910	2	T38539	probable importin	669	33	37.1	88	2	T31230	hypothetical prote
597	34	38.2	912	2	D72644	hypothetical prote	670	33	37.1	106	2	JC2267	midkine-related pr
598	34	38.2	916	2	C82844	alanyl-tRNA synth	671	33	37.1	110	2	T45387	hypothetical prote
599	34	38.2	924	2	B41359	potassium channel	672	33	37.1	120	2	S77774	probable adenyllosu
600	34	38.2	924	2	S12746	potassium channel	673	33	37.1	125	2	S28684	hypothetical prote
601	34	38.2	929	2	G72677	hypothetical prote	674	33	37.1	133	2	S73222	ribosomal protein
602	34	38.2	967	1	SYMTAT	alanine-tRNA ligas	675	33	37.1	133	2	S77489	ribosomal protein
603	34	38.2	982	2	T19526	hypothetical prote	676	33	37.1	134	1	R3NT8	ribosomal protein
604	34	38.2	1058	2	T30580	P-type ATPase - sl	677	33	37.1	140	2	A35305	retinoic acid-indu
605	34	38.2	1112	2	T30202	probable chitin sy	678	33	37.1	144	2	D84287	hypothetical prote
606	34	38.2	1114	2	T49517	p63 related protei	679	33	37.1	161	2	E48232	cysteine-rich exte
607	34	38.2	1136	2	D86190	hypothetical prote	680	33	37.1	161	2	AF0536	conserved hypothet
608	34	38.2	1231	2	S53089	protein-tyrosine-p	681	33	37.1	162	2	B81635	conserved hypothet
609	34	38.2	1256	2	G97902	alpha-amylase (EC	682	33	37.1	186	2	B70040	molybdenum transpo
610	34	38.2	1280	2	E95031	alkaline amylophil	683	33	37.1	191	2	AH5571	alpha-ribazole-5 -
611	34	38.2	1306	1	A31759	peptidyl-dipectida	684	33	37.1	192	2	D83045	hypothetical prote
612	34	38.2	1372	2	A34157	insulin receptor p	685	33	37.1	193	2	AI0018	probable membrane
613	34	38.2	1382	1	INHUR	insulin receptor p	686	33	37.1	194	1	NNKE2C	anthranilate synth

687	33	37.1	201	2	G75263	hypotheical prote	760	33	37.1	425	2	S28295	hypotheical prote
688	33	37.1	202	2	J95897	conserved hypothe	761	33	37.1	426	2	AH2144	hypotheical prote
689	33	37.1	213	2	JE0247	Ig lambda chain Ni	762	33	37.1	428	2	B64081	fucose permease ho
690	33	37.1	214	2	AB3415	outer membrane por	763	33	37.1	430	2	S55325	endo-beta-1,6-gluc
691	33	37.1	223	2	A30528	serum amyloid P-co	764	33	37.1	434	1	A35005	u-plasminogen acti
692	33	37.1	224	2	B84502	En/Spm-like transp	765	33	37.1	435	2	S52268	malate dehydrogena
693	33	37.1	224	2	AG3258	hypotheical prote	766	33	37.1	438	2	E96545	hypotheical prote
694	33	37.1	249	2	B4097	cyclase hisf limpo	767	33	37.1	444	2	E85974	probable galactara
695	33	37.1	252	2	T09031	hypotheical prote	768	33	37.1	444	2	E91129	probable galactara
696	33	37.1	258	2	T51763	2-ketocyclohexanec	769	33	37.1	444	2	C65102	hypotheical prote
697	33	37.1	260	2	F64239	Holliday junction	770	33	37.1	450	2	T37182	nitrogen fixation
698	33	37.1	260	2	A41531	TGFbeta-regulated	771	33	37.1	457	2	A13619	CAP59 protein - Cr
699	33	37.1	260	2	I46081	uroplakin Ib - bov	772	33	37.1	458	2	A56055	protein transport
700	33	37.1	267	2	I39573	probable 3-isoprop	773	33	37.1	461	2	A50520	cell cycle protein
701	33	37.1	269	2	T16487	hypotheical prote	774	33	37.1	470	2	T31485	hypotheical prote
702	33	37.1	272	2	JC5587	glutamate racemase	775	33	37.1	475	2	T48983	medium-chain-fatty
703	33	37.1	272	2	B69688	glutamate racemase	776	33	37.1	475	2	E90318	undecaprenyl-phosp
704	33	37.1	273	2	S57766	diocorin class A	777	33	37.1	477	2	S61891	conserved hypotet
705	33	37.1	286	2	A95395	protein (imported	778	33	37.1	478	2	D83043	hypotheical prote
706	33	37.1	288	2	A11966	permease protein o	779	33	37.1	482	2	T34338	probable transport
707	33	37.1	289	2	G86403	33.3K hypotheical	780	33	37.1	481	2	B85791	probable transport
708	33	37.1	293	2	G98352	dipeptide ABC tran	781	33	37.1	481	2	F90942	probable transport
709	33	37.1	293	2	AG2929	hypotheical prote	782	33	37.1	481	2	D87546	benzaldehyde dehyd
710	33	37.1	304	2	JX0209	alpha (1,3) fucosy	783	33	37.1	487	2	T47697	Regulator of chrom
711	33	37.1	304	2	I39049	En/Spm transposon	784	33	37.1	488	2	S19435	hypotheical prote
712	33	37.1	307	2	F84502	cwl protein - fis	785	33	37.1	492	2	T18789	hypotheical prote
713	33	37.1	308	2	S71746	pyruvate formate-1	786	33	37.1	496	2	S26402	hypotheical prote
714	33	37.1	320	2	E69264	probable annexin [787	33	37.1	497	2	E86485	lysyl-tRNA synthet
715	33	37.1	321	2	A84809	hypotheical prote	788	33	37.1	499	2	G98180	lysyl-tRNA synthet
716	33	37.1	322	2	AH1344	hypotheical prote	789	33	37.1	499	2	A83106	ammonium transport
717	33	37.1	322	2	AC1715	hypotheical prote	790	33	37.1	499	2	S51089	hypotheical prote
718	33	37.1	330	2	AB3267	hypotheical prote	791	33	37.1	502	2	S89637	hypotheical prote
719	33	37.1	330	2	S70127	hypotheical prote	792	33	37.1	502	2	S89637	hypotheical prote
720	33	37.1	336	2	T38175	hypotheical prote	793	33	37.1	504	2	E83980	glycine betaine tr
721	33	37.1	337	2	B71340	conserved hypotet	794	33	37.1	507	2	B87400	aldehyde dehydroge
722	33	37.1	342	2	S60386	hypotheical prote	795	33	37.1	507	2	T48645	glycine betaine tr
723	33	37.1	342	2	E82846	hypotheical prote	796	33	37.1	507	2	AB1336	glycine betaine tr
724	33	37.1	342	2	T21530	hypotheical prote	797	33	37.1	507	2	AD1707	glycine betaine tr
725	33	37.1	344	2	S62020	probable membrane	798	33	37.1	510	2	A54798	Vg-1-related prote
726	33	37.1	344	2	B42436	L-rhamnose-H+ tran	799	33	37.1	512	2	G69670	glycine betaine tr
727	33	37.1	344	2	T03499	integraser/recombin	800	33	37.1	513	1	BMH06	bone morphogenetic
728	33	37.1	347	2	B85432	hypotheical prote	801	33	37.1	514	2	T41648	C2 domain family p
729	33	37.1	348	2	S64041	probable membrane	802	33	37.1	517	2	G84136	glycine betaine tr
730	33	37.1	348	2	A71153	hypotheical prote	803	33	37.1	520	2	D90014	hypotheical prote
731	33	37.1	352	2	T33433	hypotheical prote	804	33	37.1	522	1	KJHUG6	probable membrane
732	33	37.1	352	2	T27712	hypotheical prote	805	33	37.1	546	2	AE0571	probable BCCR-fam
733	33	37.1	355	2	E64445	polyferredoxin 4x2	806	33	37.1	548	2	AG0304	transcription fact
734	33	37.1	357	2	E85049	probable transposo	807	33	37.1	556	2	T19748	hypotheical prote
735	33	37.1	358	2	S21998	envelope protein 9	808	33	37.1	558	2	A82202	hypotheical prote
736	33	37.1	359	2	A45156	alpha-(1,3)-fucosy	809	33	37.1	559	2	AE5097	neutral invertase
737	33	37.1	361	2	A36669	3-alpha-galactosyl	810	33	37.1	566	2	T37578	probable 1,3-beta-
738	33	37.1	362	2	T29552	hypotheical prote	811	33	37.1	570	2	H64075	urease (EC 3.5.1.5
739	33	37.1	364	2	I39048	alpha (1,3) fucosy	812	33	37.1	572	2	H64075	hypotheical prote
740	33	37.1	369	2	T24022	hypotheical prote	813	33	37.1	579	2	AB2177	hypotheical prote
741	33	37.1	374	2	A42270	alpha (1,3) fucosy	814	33	37.1	580	2	E86177	phosphoprotein pho
742	33	37.1	374	2	T44691	precocorrin methylas	815	33	37.1	588	2	B86385	phosphoprotein pho
743	33	37.1	379	2	T52405	hypotheical prote	816	33	37.1	588	2	S92215	hypotheical prote
744	33	37.1	384	2	T32756	hypotheical prote	817	33	37.1	589	2	T23881	hypotheical prote
745	33	37.1	392	2	S32405	MFT1 protein - yea	818	33	37.1	589	2	S41011	phosphoprotein pho
746	33	37.1	393	2	T01167	probable isocitrat	819	33	37.1	590	2	S51807	phosphoprotein pho
747	33	37.1	395	2	E90130	hypotheical prote	820	33	37.1	595	2	T02876	probable auxin tra
748	33	37.1	396	2	T22097	hypotheical prote	821	33	37.1	602	2	JU0215	protein-tyrosine k
749	33	37.1	397	2	AF2016	hypotheical prote	822	33	37.1	603	2	E71444	probable EREBP-4 -
750	33	37.1	398	2	T27670	hypotheical prote	823	33	37.1	609	2	T00904	hypotheical prote
751	33	37.1	399	2	F70937	En/Spm transposon	824	33	37.1	616	2	C86239	protein T10024.21
752	33	37.1	400	2	H84492	alanine racemase [825	33	37.1	618	2	AC0884	glutathionylspermi
753	33	37.1	401	2	AC2113	probable flavoprot	826	33	37.1	619	2	A91113	glutathionylspermi
754	33	37.1	405	2	F97340	hypotheical prote	827	33	37.1	619	2	A57538	glutathionylspermi
755	33	37.1	407	2	T24928	argininosuccinate	828	33	37.1	619	2	A57538	glutathionylspermi
756	33	37.1	410	2	T40457	phosphate regulon	829	33	37.1	635	2	T20587	hypotheical prote
757	33	37.1	412	2	AB3455	hypotheical prote	830	33	37.1	653	2	T12482	hypotheical prote
758	33	37.1	423	2	T19079	non-selective cati	831	33	37.1	656	2	AF1040	vi polysaccharide
759	33	37.1	424	2	JC5921		832	33	37.1	656	2	A56975	vi polysaccharide

833	33	37.1	661	2	G82985	probable choline t	906	32.5	36.5	109	4	S5848	hypothetical prote
834	33	37.1	669	2	T28028	hypothetical prote	907	32.5	36.5	112	2	S10918	hypothetical 12K p
835	33	37.1	695	2	F64135	carboxy-terminal p	908	32.5	36.5	116	1	S15197	hyPA protein - Esc
836	33	37.1	695	2	T38804	hypothetical WW do	909	32.5	36.5	116	2	F95921	pleiotropic effec
837	33	37.1	696	2	G88851	protein ZK929.10 l	910	32.5	36.5	116	2	F91076	Hypa protein (impo
838	33	37.1	707	2	T24361	hypothetical prote	911	32.5	36.5	128	2	G75322	hypothetical prote
839	33	37.1	708	2	T25725	hypothetical prote	912	32.5	36.5	133	2	AB2421	hypothetical prote
840	33	37.1	719	2	F96830	hypothetical prote	913	32.5	36.5	151	2	T09884	ribonuclease H XF2
841	33	37.1	725	2	JE0099	neural cell adhesi	914	32.5	36.5	151	2	F82591	hypothetical prote
842	33	37.1	741	2	A45771	2-SA-dependent RNA	915	32.5	36.5	165	2	E84451	hypothetical prote
843	33	37.1	743	2	AE3145	hypothetical prote	916	32.5	36.5	177	2	T49691	cysteine-rich exte
844	33	37.1	743	2	G83726	assimilatory nitra	917	32.5	36.5	196	2	B48232	cysteine-rich exte
845	33	37.1	747	2	F98142	iron(III) ABC tran	918	32.5	36.5	209	2	A48232	hypothetical prote
846	33	37.1	761	2	E82167	5-methyltetrahydro	919	32.5	36.5	218	2	F84170	disulfide bond for
847	33	37.1	768	2	C96545	hypothetical prote	920	32.5	36.5	242	2	AB3621	hypothetical zinc-
848	33	37.1	780	2	E69095	carbon monoxide de	921	32.5	36.5	249	2	T37669	hypothetical prote
849	33	37.1	781	2	T36143	probable secreted	922	32.5	36.5	254	2	D83446	hypothetical prote
850	33	37.1	797	2	A70453	myotubularin-like	923	32.5	36.5	291	1	UN0631	protein kinase (EC
851	33	37.1	799	2	T48451	glutamate ammonia	924	32.5	36.5	314	2	AJ2186	hypothetical prote
852	33	37.1	805	2	S68441	leptin receptor, s	925	32.5	36.5	333	1	A40548	gap junction prote
853	33	37.1	807	2	C85025	hypothetical prote	926	32.5	36.5	333	1	B42053	gap junction prote
854	33	37.1	827	2	T47797	hypothetical prote	927	32.5	36.5	333	2	I55593	connexin 37 - huma
855	33	37.1	829	2	S58241	pyrroloquinoline q	928	32.5	36.5	354	2	B70611	hypothetical prote
856	33	37.1	853	2	T51505	hypothetical prote	929	32.5	36.5	355	2	A55733	G protein-coupled
857	33	37.1	854	2	A96574	protein F12M16.30	930	32.5	36.5	358	2	A53752	interleukin-8 rece
858	33	37.1	861	1	VCLJKB	env polyprotein pr	931	32.5	36.5	360	2	A53611	interleukin-8 rece
859	33	37.1	878	2	A69584	alanine-tRNA ligas	932	32.5	36.5	365	2	A30891	regulatory protein
860	33	37.1	891	2	G75014	valyl-tRNA synthet	933	32.5	36.5	385	2	S53718	homoeostic protein d
861	33	37.1	892	2	S68439	leptin receptor, s	934	32.5	36.5	385	2	A54785	predipocyte facto
862	33	37.1	894	2	S68437	leptin receptor, s	935	32.5	36.5	410	2	T50980	hypothetical prote
863	33	37.1	895	2	S74225	leptin receptor, i	936	32.5	36.5	457	2	S50357	sugar transport pr
864	33	37.1	896	2	D71457	valine-tRNA ligase	937	32.5	36.5	459	2	B95031	glycosyl hydrolase
865	33	37.1	900	2	S68440	leptin receptor, s	938	32.5	36.5	459	2	D87902	beta-glucosidase h
866	33	37.1	926	2	A54142	nucleoporin NUP107	939	32.5	36.5	464	2	AG1146	beta-glucosidase h
867	33	37.1	946	2	S71168	hypothetical prote	940	32.5	36.5	465	2	AG1505	hypothetical prote
868	33	37.1	950	2	F86222	macrophage colony-	941	32.5	36.5	475	2	H84137	hypothetical prote
869	33	37.1	975	2	T30816	Zwille protein (im	942	32.5	36.5	480	2	AE1121	beta-glucosidase h
870	33	37.1	988	2	T52134	hypothetical prote	943	32.5	36.5	480	2	AH1481	beta-glucosidase h
871	33	37.1	999	2	T27628	hypothetical prote	944	32.5	36.5	480	2	AH1481	beta-glucosidase h
872	33	37.1	1007	2	E72489	hypothetical prote	945	32.5	36.5	490	2	T36920	hypothetical prote
873	33	37.1	1008	2	G82732	hypothetical prote	946	32.5	36.5	540	2	JG0174	phospholipase D (E
874	33	37.1	1016	2	S30236	genome polyprotein	947	32.5	36.5	567	2	S49708	hexose transport p
875	33	37.1	1020	2	D86402	protein envelope C	948	32.5	36.5	567	2	S49600	glucose transport
876	33	37.1	1020	2	T51925	Ca2+-transporting	949	32.5	36.5	615	2	G83419	probable binding p
877	33	37.1	1020	2	T51926	Ca2+-transporting	950	32.5	36.5	642	2	D88951	protein C38C3.7 (i
878	33	37.1	1033	2	T49179	Ca2+-transporting	951	32.5	36.5	667	2	B84256	acetyl-CoA synthet
879	33	37.1	1078	2	A56715	calcium receptor (952	32.5	36.5	730	2	F87803	RNA-directed DNA p
880	33	37.1	1087	2	AC3239	DNA polymerase III	953	32.5	36.5	860	2	S55543	hypothetical prote
881	33	37.1	1088	1	IJXLNL	neural cell adhesi	954	32.5	36.5	929	2	S75098	receptor kinase-li
882	33	37.1	1088	2	B56715	calcium receptor (955	32.5	36.5	1009	2	T45645	sodium channel alp
883	33	37.1	1092	2	T12520	hypothetical prote	956	32.5	36.5	1034	2	S80051	sodium channel alp
884	33	37.1	1100	2	A35007	ATP citrate (pro-S	957	32.5	36.5	1034	2	S60060	ascites siialoglyco
885	33	37.1	1102	2	S44772	C29B4.4 protein -	958	32.5	36.5	1630	2	A53577	sodium channel pro
886	33	37.1	1102	2	T12681	hypothetical prote	959	32.5	36.5	1820	2	A33299	sodium channel pro
887	33	37.1	1114	2	T18197	reverse transcript	960	32.5	36.5	2108	2	S72458	hypothetical prote
888	33	37.1	1125	2	T39052	hypothetical serin	961	32	36.0	42	2	T07581	hypothetical prote
889	33	37.1	1162	2	PC4184	leptin receptor, O	962	32	36.0	60	2	G82529	depressant insect-
890	33	37.1	1162	2	S68438	leptin receptor, s	963	32	36.0	62	2	D59352	hypothetical prote
891	33	37.1	1182	2	S14916	hypothetical prote	964	32	36.0	65	2	E83492	hypothetical prote
892	33	37.1	1189	2	AH2154	WD-repeat protein	965	32	36.0	77	2	E82617	glutaredoxin 3 - S
893	33	37.1	1229	2	S42391	SIP3 protein - yea	966	32	36.0	88	2	S77429	glutaredoxin (impo
894	33	37.1	1273	2	AF2421	hypothetical prote	967	32	36.0	90	2	A82288	chitinase - Strept
895	33	37.1	1429	2	T41699	C2-domain family p	968	32	36.0	90	2	T36400	hypothetical prote
896	33	37.1	1661	2	S64800	probable membrane	969	32	36.0	93	2	AB2212	hypothetical prote
897	33	37.1	1817	2	AD2165	two-component hybr	970	32	36.0	102	2	T49651	hypothetical prote
898	33	37.1	1896	2	B72175	D15R protein - var	971	32	36.0	104	2	S09780	hypothetical prote
899	33	37.1	1998	2	T13009	hypothetical prote	972	32	36.0	108	2	F82598	hypothetical prote
900	33	37.1	2330	1	RR1MWV	genome polyprotein	973	32	36.0	108	2	E71143	hypothetical prote
901	33	37.1	2331	2	S44054	genome polyprotein	974	32	36.0	109	2	S07509	gene 4.2 protein -
902	33	37.1	2531	2	T16743	hypothetical prote	975	32	36.0	113	2	T12933	hypothetical prote
903	33	37.1	3071	2	T45584	hypothetical prote	976	32	36.0	114	2	A70374	conserved hypothet
904	33	37.1	3343	2	T42207	breast cancer susc	977	32	36.0	116	2	S73442	hypothetical prote
905	33	37.1	3562	2	A47171	chondroitin sulfat	978	32	36.0	124	2	S57715	chitinase (EC 3.2.

A:Gene: CESP:F23B2.12
A:Map position: 4
A:Introns: 19/2; 127/2; 287/3; 349/1; 658/2; 916/2
C:Keywords: duplication

Query Match 51.7%; Score 46; DB 2; Length 1080;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
DB 886 LLWTWQTC 893

RESULT 5
T21303
hypothetical protein F23B2.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A:Accession: T21303
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19403
A:Accession: T21303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1121 <WIL>
A:CROSS-references: UNIPROT:O02252; UNIPARC:UPI0000060PBF; EMBL:Z82266; PIDN:CA805185.1;
A:Experimental source: clone F23B2
C:Genetics:
A:Gene: CESP:F23B2.11
A:Map position: 4
A:Introns: 40/2; 170/2; 330/3; 392/1; 701/2; 958/2

Query Match 51.7%; Score 46; DB 2; Length 1121;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
DB 928 LLWTWQTC 935

RESULT 6
S47466
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Clostridium thermocellum
C:Species: Clostridium thermocellum
C:Date: 23-Nov-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
A:Accession: S47466
R:Zverlov, V.V.
submitted to the EMBL Data Library, August 1994
A:Reference number: S47466
A:Accession: S47466
A:Status: preliminary
A:Molecule type: DNA
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F:1169-1192/Domain: Clostridium cellulase repeat homology <CCR2>
F:1201-1224/Domain: Clostridium cellulase repeat homology <CCR1>

Query Match 51.7%; Score 46; DB 2; Length 1230;
Best Local Similarity 63.6%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EYLCWTWETCE 12
DB 50 EYLCYVWHTCE 60

RESULT 7
A53294
superoxide dismutase (EC 1.15.1.1) (Mn) - Pseudomonas aeruginosa

C:Species: Pseudomonas aeruginosa
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
A:Accession: A53294; JC4981
R:Hassett, D.J.; Woodruff, W.A.; Wozniak, D.J.; Vasil, M.L.; Cohen, M.S.; Ohman, D.E.
J. Bacteriol. 175, 7658-7665, 1993
A:Title: Cloning and characterization of the pseudomonas aeruginosa sodA and sodB genes
dismutase activity in alginate-producing bacteria.
A:Reference number: A53294; MUID:94064560; PMID:8244935
A:Accession: A53294
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-203 <HAS>
A:CROSS-references: UNIPROT:P53652; UNIPARC:UPI00001752BD; GB:I25672
R:Polack, B.; Dacheux, D.; Delic-Attree, I.; Toussaint, B.; Vignais, P.M.
Biochem. Biophys. Res. Commun. 226, 555-560, 1996
A:Title: The Pseudomonas aeruginosa fmc and soda genes belong to an iron-responsive op
A:Reference number: JC4981; MUID:96400296; PMID:8806672
A:Accession: JC4981
A:Molecule type: DNA
A:Residues: 1-41, 'ALEGTPYAEQPVESLLRQLAGLPE', 66-203 <POL>
A:CROSS-references: UNIPARC:UPI0000135CF; GB:U72494; NID:g1628609; PIDN:AAB17391.1; PI
A:Experimental source: strain CHA
C:Genetics:
A:Gene: soda; Mn-SOD
C:Complex: homodimer
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C:Superfamily: superoxide dismutase (Mn)
C:Keywords: homodimer; manganese; metalloprotein; oxidoreductase
F:27.81,164,168/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 49.4%; Score 44; DB 2; Length 203;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
DB 53 WKVCCGNLVCRR 65

RESULT 8
T10000
cytochrome P450 (CYP72C)- Madagascar periwinkle (fragment)
C:Species: Catharanthus roseus (Madagascar periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-Oct-2004
A:Accession: T10000
R:Mangold, U.; Eichel, J.; Batschauer, A.; Lanz, T.; Kaiser, T.; Spangenberg, G.; Werck
Plant Sci. 96, 129-136, 1994
A:Title: Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from Catharan.
A:Reference number: Z16915
A:Accession: T10000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-516 <MAN>
A:CROSS-references: UNIPROT:Q42701; UNIPARC:UPI00000A2837; EMBL:L19075; NID:g404689; PI
A:Experimental source: cv. cp3
C:Genetics:
A:Gene: CYP72C
C:Keywords: heme; iron; metalloprotein
F:318-481/Domain: cytochrome P450 homology <P45>
F:459/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 516;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
DB 14 WRVLDNAWFTPKR 26

RESULT 9
T09999

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woose, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69373
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-347 <KLE>
A:Cross-references: UNIPROT:Q29274; UNIPARC:UPI0000056ED9; GB:AE001036; GB:AE000782; NID
C:Superfamily: immunogenic protein BCSP31

Query Match 47.2%; Score 42; DB 2; Length 347;
Best Local Similarity 54.5%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCE 12
DB 35 EVKPKSWATCD 45
||| :||| :
||| :||| :

RESULT 12
T45766
hypothetical protein F24M12.390 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45766
R:Vitala, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23012
A:Accession: T45766
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <VIT>
A:Cross-references: UNIPROT:Q9SD14; UNIPARC:UPI0000179697; EMBL:AL132980
A:Experimental source: cultivar Columbia; BAC clone F24M12
C:Genetics:
A:Map position: 3
A:Introns: 100/2; 147/3; 225/2; 302/2; 319/2; 356/3; 375/3; 399/1
A:Note: F24M12.390
C:Superfamily: Arabidopsis thaliana hypothetical protein F24M12.380

Query Match 47.2%; Score 42; DB 2; Length 475;
Best Local Similarity 60.0%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLCWTWETCE 12
DB 15 VVCWGFERCE 24
||| :||| :
||| :||| :

RESULT 13
E85025
hypothetical protein AT4g01990 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85025
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: E85025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: UNIPROT:Q9SYJ6; UNIPARC:UPI00000A1D96; GB:NC_001268; NID:g7268583; I
C:Genetics:
A:Gene: AT4g01990
A:Map position: 4

Query Match 47.2%; Score 42; DB 2; Length 501;
Best Local Similarity 55.6%; Pred. No. 99;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCTWE 9
|||
341 WESTCWTYD 349

Db

RESULT 14
S75169
urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1750
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75169
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75169
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-569 <XAN>
A:Cross-references: UNIPROT:P73061; UNIPARC:UPI0000137D79; EMBL:D90903; GB:AB001339; NID F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
C:Genetics:
A:Gene: ureC
C:Superfamily: urease, alpha subunit; urease 62K chain homology
C:Keywords: hydrolase; metalloprotein; nickel
F:552/Domain: urease 62K chain homology <U62>
F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 47.2%; Score 42; DB 2; Length 569;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCTWETCER 13
|||
371 EVICTWQTAHK 382

Db

RESULT 15
T09172
probable calcium-activated potassium channel KCNN3 - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T09172
R:Chandry, K.G.; Fantino, E.; Wittekindt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman, G Mol. Psychiatry 3, 32-37, 1998
A:Title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic CAG A:Reference number: Z16601; MUID:98150774; PMID:9491810
A:Accession: T09172
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-731 <CHA>
A:Cross-references: UNIPROT:Q96DJ3; UNIPARC:UPI00001696F1; EMBL:AF031815; NID:G3309530;
C:Genetics:
A:Gene: KCNN3
C:Keywords: potassium channel; schizophrenia

Query Match 47.2%; Score 42; DB 2; Length 731;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
471 WIIAATVTRACER 483

Db

RESULT 16
A22421
3-dehydroshikimate dehydratase - Neurospora crassa
C:Species: Neurospora crassa

QY 1 WEVLCTWE 9
|||
341 WESTCWTYD 349

Db

RESULT 14
S75169
urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1750
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75169
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yanada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75169
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-569 <XAN>
A:Cross-references: UNIPROT:P73061; UNIPARC:UPI0000137D79; EMBL:D90903; GB:AB001339; NID F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
C:Genetics:
A:Gene: ureC
C:Superfamily: urease, alpha subunit; urease 62K chain homology
C:Keywords: hydrolase; metalloprotein; nickel
F:552/Domain: urease 62K chain homology <U62>
F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 47.2%; Score 42; DB 2; Length 569;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCTWETCER 13
|||
371 EVICTWQTAHK 382

Db

RESULT 15
T09172
probable calcium-activated potassium channel KCNN3 - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T09172
R:Chandry, K.G.; Fantino, E.; Wittekindt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman, G Mol. Psychiatry 3, 32-37, 1998
A:Title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic CAG A:Reference number: Z16601; MUID:98150774; PMID:9491810
A:Accession: T09172
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-731 <CHA>
A:Cross-references: UNIPROT:Q96DJ3; UNIPARC:UPI00001696F1; EMBL:AF031815; NID:G3309530;
C:Genetics:
A:Gene: KCNN3
C:Keywords: potassium channel; schizophrenia

Query Match 47.2%; Score 42; DB 2; Length 731;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCTWETCER 13
|||
471 WIIAATVTRACER 483

Db

RESULT 16
A22421
3-dehydroshikimate dehydratase - Neurospora crassa
C:Species: Neurospora crassa

C:Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 12-Jul-2004
C:Accession: A22421; S04252; D31277
R:Rutledge, B.J.
Gene 32, 275-287, 1984
A:Title: Molecular characterization of the qa-4 gene of Neurospora crassa.
A:Reference number: A22421; MUID:85155494; PMID:6241580
A:Accession: A22421
A:Molecule type: DNA
A:Residues: 1-359 <RUT>
A:Cross-references: UNIPROT:P07046; UNIPARC:UPI0000124EFE; GB:M10139; NID:G168877; PIDN A:Note: the authors translated the codon GAC for residue 93 as Glu, GGC for residue 9 4 Leu, GCA for residue 99 as Glu, GAA for residue 100 as Lys, CAT for residue 101 as Leu, AAG for residue 107 as Leu, CTA for residue 108 as
A:Note: ala, GCA for residue 109 as His, CTA for residue 110 as Glu, TGG for residue 11 5 as Asp, CAT for residue 116 as Arg, and GAG for residue 117 as Ala
R:deever, R.F.; Huet, L.; Rutledge, B.J.; Tyler, B.M.; Patel, V.B.; Rutledge, B.J.; Case, J. Mol. Biol. 107, 15-34, 1989
A:Title: DNA sequence, organization and regulation of the qa gene cluster of Neurospora A:Reference number: S04250; MUID:89293848; PMID:2525625
A:Accession: S04252
A:Molecule type: DNA
A:Residues: 1-359 <GEE>
A:Cross-references: UNIPARC:UPI0000124EFE; EMBL:X14603; NID:G3060; PIDN:CAA32750.1; PID C:Genetics:
A:Gene: qa-4
C:Superfamily: 3-dehydroshikimate dehydratase

Query Match 46.6%; Score 41.5; DB 2; Length 359;
Best Local Similarity 43.8%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 1 WEVLCTWE 11
|||
164 YESLCWSTRVLUWERC 179

Db

RESULT 17
S36808
methylmalonyl-CoA carboxyltransferase (EC 2.1.3.1) 5S chain [validated] - Propionibacte: N:Alternate names: transcarboxylase 5S chain
C:Species: Propionibacterium freudenreichii subsp. shermanii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S36808; S77738; A28895
R:Thornton, C.G.; Kumar, G.K.; Shenoy, B.C.; Haase, F.C.; Phillips, N.F.B.; Park, V.M.; FEBS Lett. 330, 191-196, 1993
A:Title: Primary structure of the 5 subunit of transcarboxylase as deduced from the g A:Reference number: S36808; MUID:93374062; PMID:8365490
A:Accession: S36808
A:Molecule type: DNA
A:Residues: 1-519 <THO1>
A:Cross-references: UNIPROT:Q05618; UNIPARC:UPI00000BE7CD; EMBL:L06488; NID:G150928; PI A:Experimental source: strain ST33
A:Note: the source is designated as Propionibacterium shermanii
A:Accession: S77738
A:Molecule type: protein
A:Residues: 3-22; 67-88-92; 111-124; 134-147; 301-312; 321-333; 368-390; 415-428; 448-473 <T A:Cross-references: UNIPARC:UPI0000176286; UNIPARC:UPI0000176287; UNIPARC:UPI000017628 28D; UNIPARC:UPI000017628E; UNIPARC:UPI000017628F.
R:Kumar, G.K.; Haase, F.C.; Phillips, N.F.B.; Wood, H.G. Biochemistry 27, 5978-5983, 1988
A:Title: Involvement and identification of a tryptophanyl residue at the pyruvate bindi A:Reference number: A28895; MUID:89050938; PMID:3191103
A:Accession: A28895
A:Molecule type: protein
A:Residues: 67-75 <KUM>
A:Cross-references: UNIPARC:UPI0000176290
A:Note: the strain or subspecies was not identified
C:Genetics:
A:Gene: 58
C:Superfamily: Propionibacterium methylmalonyl-CoA carboxyltransferase 5S chain
C:Keywords: biotin metabolism; transferase
F:73/Binding site: substrate (Trp) #status predicted

Query Match 46.6%; Score 41.5; DB 2; Length 519;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

OY 1 WEVLCW---TWETCER 13
DB 51 WSVECMGGATYDSCIR 66

RESULT 18
E71621
ERCC1-like excision repair protein PFB0160w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: E71621
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Partea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: E71621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-242 <GAR>
A:Cross-references: UNIPROT:O96136; UNIPARC:UPI0000080071; GB:AE001377; GB:AE001362; NID
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0160w

Query Match 46.1%; Score 41; DB 2; Length 242;
Best Local Similarity 54.5%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 VLCWTWETCER 13
DB 144 ILCWNEECAR 154

RESULT 19
T47351
hypothetical protein F18p9.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47351
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24458
A:Accession: T47351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <NYA>
A:Cross-references: UNIPROT:Q9M1L2; UNIPARC:UPI00000A5EAC; EMBL:AL138654
A:Experimental source: cultivar Columbia; BAC clone F18p9
C:Genetics:
A:Map position: 3
A:Introns: 21/1; 107/3; 161/3
A:Notes: F18p9.90

Query Match 46.1%; Score 41; DB 2; Length 276;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 WEVLCWTWETCE 12
DB 58 WETWCAYWTEE 69

RESULT 20
S48776
hypothetical protein YDR087c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4478; hypothetical protein YD8554.20c
C:Species: Saccharomyces cerevisiae

Query Match 46.1%; Score 41; DB 2; Length 278;
Best Local Similarity 38.5%; Pred. No. 81;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WEVLCWTWETCER 13
DB 103 WKVMCFEWFNIDR 115

RESULT 21
A75316
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75316
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <WHI>

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S48776; S49842; S39583; S55836; S67904
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48758
A:Accession: S48776
A:Molecule type: DNA
A:Residues: 1-278 <COS>
A:Cross-references: UNIPROT:P35178; UNIPARC:UPI0000052F16; EMBL:X82086; NID:G558241; PID
R:Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49823
A:Accession: S49842
A:Molecule type: DNA
A:Residues: 1-278 <RIC>
A:Cross-references: UNIPARC:UPI0000052F16; EMBL:Z46796; NID:G577794; PIDN:CAA86809.1; PI
EMBO J. 12, 4083-4093, 1993
R:Esnaul, Y.; Blondel, M.O.; Deshaies, R.J.; Schekman, R.; Kepes, F.
A:Title: The yeast S81 gene is essential for secretory protein translocation and encode
A:Reference number: S39583; MUID:94038890; PMID:8223425
A:Accession: S39583
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 146-278 <ESN>
A:Cross-references: UNIPARC:UPI0000168ESD; EMBL:X74499; NID:G414690; PIDN:CAA52607.1; PI
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr
A:Reference number: S55819; MUID:96093910; PMID:7483840
A:Accession: S55836
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-278 <COW>
A:Cross-references: UNIPARC:UPI0000052F16; EMBL:X82086; NID:G558241; PIDN:CAA57616.1; PI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
R:Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67889
A:Accession: S67904
A:Molecule type: DNA
A:Residues: 1-278 <FOU>
A:Cross-references: UNIPARC:UPI0000052F16; EMBL:Z74383; NID:G1431562; PIDN:CAA98907.1; F
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD.RRP1
A:Cross-references: SGD:S0002494
A:Map position: 4R

Query Match 46.1%; Score 41; DB 2; Length 278;
Best Local Similarity 38.5%; Pred. No. 81;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 WEVLCWTWETCER 13
DB 103 WKVMCFEWFNIDR 115

RESULT 21
A75316
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75316
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <WHI>

A;Cross-references: UNIPROT:Q9RSM5; UNIPARC:UPI00000C1A6B; GB:AE002045; GB:AE000513; NID:10036
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2099
A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical protein DR2099

Query Match 46.1%; Score 41; DB 2; Length 306;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 3 VLCWTWE 9
DB 206 VTCWTWQ 212

RESULT 22
S08500
QUTG protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S08500; S11944
R;Hawkins, A.R.; Lamb, H.K.; Smith, M.; Keyte, J.W.; Roberts, C.F.
Mol. Gen. Genet. 214, 224-231, 1988
A;Title: Molecular organisation of the quinic acid utilization (QUT) gene cluster in *Aspergillus nidulans*
A;Reference number: S08498; MUID:89181521; PMID:2976880
A;Accession: S08500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <HAW>
A;Cross-references: UNIPROT:P25416; UNIPARC:UPI0000132EA5; EMBL:X13525; NID:g2398; PID:g2398
A;Note: the authors translated the codon GCG for residue 327 as Thr
R;Lamb, H.K.; Hawkins, A.R.; Smith, M.; Harvey, I.J.; Brown, J.; Turner, G.; Roberts, C.
Mol. Gen. Genet. 223, 17-23, 1990
A;Title: Spatial and biological characterisation of the complete quinic acid utilisation
A;Reference number: S11944; MUID:91080861; PMID:2175387
A;Accession: S11944
A;Molecule type: DNA
A;Residues: 1-326, 'T' <LAMS>
A;Cross-references: UNIPARC:UPI000017B3DF
A;Experimental source: strain 2035
C;Genetics:
A;Introns: 57/1; 104/1; 250/2; 293/2

Query Match 46.1%; Score 41; DB 2; Length 330;
Best Local Similarity 55.6%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
DB 243 WEGGCWEWD 251

RESULT 23
B31277
hypothetical protein qa-x - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 09-Jul-2004
C;Accession: S04250; B31277
R;Geever, R.F.; Huillet, L.; Baum, J.A.; Tyler, B.M.; Patel, V.B.; Rutledge, B.J.; Case, M.
J. Mol. Biol. 207, 15-34, 1989
A;Title: DNA sequence, organization and regulation of the qa gene cluster of *Neurospora crassa*
A;Reference number: S04250; MUID:89293848; PMID:2525625
A;Accession: S04250
A;Molecule type: DNA
A;Residues: 1-340 <GEE>
A;Cross-references: UNIPROT:P11634; UNIPARC:UPI0000132E4A; EMBL:X14603; NID:g3060; PID:n3060
C;Genetics:
A;Gene: qa-x
A;Introns: 237/2; 261/2

Query Match 46.1%; Score 41; DB 2; Length 340;
Best Local Similarity 55.6%; Pred. No. 97;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
DB 254 WEGGCWEWD 262

RESULT 24
T10036
hypothetical protein MLCB628.17c - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T10036
R;Biglmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.
Mol. Microbiol. 7, 197-206, 1993
A;Title: Use of an ordered cosmid library to deduce the genomic organization of *Mycobacterium leprae*
A;Reference number: Z16917; MUID:93188700; PMID:8446027
A;Accession: T10036
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-481 <EIG>
A;Cross-references: UNIPROT:O33088; UNIPARC:UPI00000D4383; EMBL:Y14967; NID:g2370268; P:10036
C;Genetics:
A;Note: MLCB628.17c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1782

Query Match 46.1%; Score 41; DB 2; Length 481;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
DB 341 YPTLCWANE 349

RESULT 25
T16658
hypothetical protein R02F2.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16658
R;Pauley, A.
submitted to the EMBL Data Library, May 1994
A;Description: The sequence of *C. elegans* cosmid R02F2.
A;Reference number: Z18555
A;Accession: T16658
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-494 <PAU>
A;Cross-references: UNIPROT:Q21652; UNIPARC:UPI0000079B27; EMBL:U00055; NID:g485143; P:10036
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:R02F2.8
A;Introns: 11/3; 92/2; 256/1; 325/1; 357/3; 406/2; 458/1

Query Match 46.1%; Score 41; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LCWTWE 9
DB 75 LCWTWK 80

RESULT 26
A96766
unknown protein F2p9.28 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A96766
R;Thologias, A.; Ecker, J.R.; Palm, C.J.; Federpsiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96766
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-575 <STO>
 A:CROSS-references: UNIPROT:Q9C9A7; UNIPARC:UPI00000A3C65; GB:AE005173; NID:g7109486; PI
 C:Genetics:
 A:Gene: F2P9.28
 A:Map position: 1

Query Match 46.1%; Score 41; DB 2; Length 575;
 Best Local Similarity 46.2%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLQWTWCER 13
 ||| : |||
 DB 322 WEALSWYKNER 334

RESULT 27
 D71347
 conserved hypothetical protein TP0263 - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: D71347
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 raon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, R.; McDo
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: D71347
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-594 <COL>
 A:CROSS-references: UNIPROT:Q83287; UNIPARC:UPI00000C0A56; GB:AE001207; GB:AE000520; NID
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0263

Query Match 46.1%; Score 41; DB 2; Length 594;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CWTWCER 13
 ||| : |||
 DB 37 CTWELCER 45

RESULT 28
 AD0014
 primosomal protein n' [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD0014
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AD0014
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-732 <KOR>
 A:CROSS-references: UNIPROT:Q8ZJUL; UNIPARC:UPI00000DC7B9; GB:AL590842; PIDN:CAC88974.1;

C:Genetics:
 A:Gene: pria

Query Match 46.1%; Score 41; DB 2; Length 732;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTWE 9
 | : |||
 DB 78 WRILCWATE 86

RESULT 29

G96814
 hypothetical protein T30F21.6 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: G96814
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96814
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-856 <STO>
 A:CROSS-references: UNIPROT:Q9SYM1; UNIPARC:UPI000009DB5C; GB:AE005173; NID:g4836872; PI
 C:Genetics:
 A:Gene: T30F21.6
 A:Map position: 1

Query Match 46.1%; Score 41; DB 2; Length 856;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTWET 10
 ||| : |||
 DB 271 WELQLKWES 280

RESULT 30

T00260
 hypothetical protein KIAA0605 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C:Accession: T00260
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
 A:Reference number: Z14086; MUID:98290545; PMID:9628581
 A:Accession: T00260
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-951 <NAG>
 A:CROSS-references: UNIPROT:Q60345; UNIPARC:UPI000006E1FB; EMBL:AB011177; NID:g3043733;
 A:Experimental source: brain
 C:Genetics:
 A:Note: KIAA0605
 F:46-106/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 46.1%; Score 41; DB 2; Length 951;
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTW 8
 | : |||

Db 5 WQCSCHAW 12

RESULT 31
H82511
hypothetical protein VCA0020 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82511
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: H82511
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1085 <HEI>
A:Cross-references: UNIPROT:Q9KNES; UNIPARC:UPI00000C33CA; GB:AE004345; GB:AE003853; NID:
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Map position: 2

Query Match 46.1%; Score 41; DB 2; Length 1085;
Best Local Similarity 71.4%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WTWETCE 12
||| |||
Db 144 WTWRVCE 150

RESULT 32
T21432
hypothetical protein F26H11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21432
R:Barlow, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19421
A:Accession: T21432
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1711 <WIL>
A:Cross-references: UNIPROT:O45409; UNIPARC:UPI000007D4BC; EMBL:Z81515; PIDN:CAB04197.1;
A:Experimental source: clone F26H11
C:Genetics:
A:Gene: CESP:F26H11.2
A:Map position: 2
A:Introns: 56/3; 154/2; 373/2; 417/3; 505/2; 596/1; 703/2; 847/3; 922/3; 1034/2; 1078/2;

Query Match 46.1%; Score 41; DB 2; Length 1711;
Best Local Similarity 71.4%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWET 10
||| |||
Db 1075 LCKWQWT 1081

RESULT 33
T47325
hypothetical protein T12K4.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47325
R:Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Rudd, S.; Lemcke, K.; May
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24460
A:Accession: T47325

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1256 <MON>
A:Cross-references: UNIPROT:Q9M297; UNIPARC:UPI00000AB305; EMBL:AL138640
A:Experimental source: cultivar Columbia; BAC clone T12K4
C:Genetics:
A:Map position: 3
A:Introns: 17/1; 94/3; 566/3; 612/3
A:Note: T12K4.120

Query Match 45.5%; Score 40.5; DB 2; Length 1256;
Best Local Similarity 53.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 WEVLQW-TWETCE 12
:||| ||| |||
Db 18 FEVFCWGTWAVE 30

RESULT 34
S71752
giant protein p619 - human
N:Alternate names: chromosome condensation regulator RCC1 homolog p619
C:Species: Homo sapiens (man)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71752
R:Rosa, J.L.; Casaroli-Marano, R.P.; Buckler, A.J.; Vilaro, S.; Barbacid, M.
EMBO J. 15, 4262-4273, 1996
A:Title: p619, a giant protein related to the chromosome condensation regulator RCC1, is
A:Reference number: S71752; MUID:97015127; PMID:8861955
A:Accession: S71752
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-4861 <ROS>
A:Cross-references: UNIPROT:Q15751; UNIPARC:UPI00001100FE; EMBL:U50078; NID:g4220427; P:
C:Genetics:
A:Gene: p619
C:Function:
A:Description: may play an important role in the regulation of membrane trafficking; shu
C:Superfamily: human giant protein p619; ubiquitin-protein ligase homology; WD repeat h
C:Keywords: leucine zipper
F:1771-1805/Region: leucine zipper motif
F:3424-3457/Domain: WD repeat homology <WD1>
F:3743-3776/Domain: WD repeat homology <WD2>
F:4484-4838/Domain: ubiquitin-protein ligase homology <UBI>

Query Match 45.5%; Score 40.5; DB 2; Length 4861;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 8; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 2 EVLQW-TWETCE 12
||| ||| |||
Db 2960 EVLDWPTWVCE 2971

RESULT 35
A70513
hypothetical protein Rv2118c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2004
C:Accession: A70513
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70513
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-280 <COL>
A:Cross-references: UNIPROT:O33253; UNIPARC:UPI00000D115F; GB:Z97559; GB:AL123456; NID:

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: RV2118c

C;Superfamily: tRNA methyltransferase, GCD14 type

Query Match 44.9%; Score 40; DB 2; Length 280;

Best Local Similarity 53.8%; Pred. No. 1.1e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 5 CWT---WETCER 13

||| ||| ||| |||

Db 221 CWTEPRAWETLQR 233

RESULT 36

S46749

hypothetical protein YHR046c - yeast (Saccharomyces cerevisiae)

A;Alternate names: hypothetical protein H8179.23

C;Species: Saccharomyces cerevisiae

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004

C;Accession: S46749

R;Du Z.

submitted to the EMBL Data Library, May 1994

A;Description: The sequence of S. cerevisiae cosmid 8179.

A;Reference number: S46732

A;Accession: S46749

A;Molecule type: DNA

A;Residues: 1-295 <DUZ>

A;Cross-references: UNIPROT:P38710; UNIPARC:UPI000013B2A3; EMBL:U00062; NID:g488162; PII

C;Genetics:

A;Gene: MIPS:YHR046c

A;Cross-references: SGD:S0001088

A;Map position: 8R

C;Superfamily: suppressor protein subB

Query Match 44.9%; Score 40; DB 2; Length 295;

Best Local Similarity 36.4%; Pred. No. 1.2e+02;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTWETC 11

||| ||| ||| |||

Db 223 WDGGCYSDVC 233

RESULT 37

D87531

glycosyl transferase family protein CC2277 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: D87531

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: D87531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-306 <STO>

A;Cross-references: UNIPROT:Q9A618; UNIPARC:UPI00000C7689; GB:AE005673; NID:gl3423792; F

C;Genetics:

A;Gene: CC2277

C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase

Query Match 44.9%; Score 40; DB 2; Length 306;

Best Local Similarity 55.6%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLQWTWE 9

||| ||| ||| |||

Db 202 WEPAAWWE 210

RESULT 38

T49840

hypothetical protein B24H17.260 [imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T49840

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49840

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-415 <SCH>

A;Cross-references: UNIPROT:Q9P519; UNIPARC:UPI000006A058; EMBL:AL356815; GSPDB:GN00116;

A;Experimental source: BAC clone B24H17; strain OR74A

C;Genetics:

A;Gene: NCSP:B24H17.260

A;Map position: 6

A;introns: 65/2

Query Match 44.9%; Score 40; DB 2; Length 415;

Best Local Similarity 40.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTWET 10

||| ||| ||| |||

Db 391 WSLVAWEWES 400

RESULT 39

G86232

cysteine proteinase (EC 3.4.22.-) [similarity] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: G86232

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: G86232

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-416 <STO>

A;Cross-references: UNIPROT:O04507; UNIPARC:UPI000009D109; GB:AE005172; NID:g2160175; P1

C;Genetics:

A;Map position: 1

C;Superfamily: papain

C;Keywords: cysteine proteinase; hydrolase

F:140,283,303/Active site: Cys, His, Asn #status predicted

Query Match 44.9%; Score 40; DB 2; Length 416;

Best Local Similarity 55.6%; Pred. No. 1.6e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETCER 12

||| ||| ||| |||

Db 376 LCFSWKCE 384

RESULT 40

T19963

hypothetical protein C46C2.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19963

R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19204
A:Accession: T19963
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-614 <WIL>
A:Cross-references: UNIPROT:Q18656; UNIPARC:UPI0000078353; EMBL:Z68296; PIDN:CAA92590.1
A:Experimental source: clone C46C2
C:Genetics:
A:Gene: CESP:C46C2.4
A:Map position: 4
A:Introns: 14/3; 78/2; 118/1; 199/3; 262/2; 426/3; 479/2; 516/3

Query Match 44.9%; Score 40; DB 2; Length 614;
Best Local Similarity 62.8%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
| | | | |
450 LLWMWQTC 457

Db

RESULT 41
B49555
enhancer of split homolog R-esp2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Oct-2004
C:Accession: B49555
R:Schmidt, C.J.; Sladek, T.E.
J. Biol. Chem. 268, 25681-25686, 1993
A:Title: A rat homolog of the Drosophila enhancer of split (groucho) locus lacking WD-40
A:Reference number: A49555; MUID:94064640; PMID:8245004
A:Accession: B49555
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-741 <SCH>
A:Cross-references: UNIPROT:Q07141; UNIPARC:UPI000013703C; GB:L14463; NID:G294548; PIDN:
A:Note: authors translated the codon TCC for residue 176 as Tyr, also Ala was found at P
F:497-530/Domain: WD repeat homology <WD1>
F:583-616/Domain: WD repeat homology <WD2>
F:665-698/Domain: WD repeat homology <WD3>
F:706-739/Domain: WD repeat homology <WD4>

Query Match 44.9%; Score 40; DB 2; Length 741;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLCWTWETC 11
| | | | |
107 LUTWWSAC 115

Db

RESULT 42
T29775
hypothetical protein C50F2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29775
R:Du, Z.; Le, T.T.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid C50F2.
A:Reference number: Z20684
A:Accession: T29775
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-855 <DUZ>
A:Cross-references: UNIPROT:P91175; UNIPARC:UPI00000788A7; EMBL:U80445; PIDN:AAB37794.1
A:Experimental source: strain Bristol N2; clone C50F2
C:Genetics:
A:Gene: CESP:C50F2.3
A:Map position: 1
A:Introns: 22/3; 62/3; 281/3; 339/2; 598/1; 634/3

Query Match 44.9%; Score 40; DB 2; Length 855;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCWTWETC 11
| | | | |
99 WRALCDTYERC 109

Db

RESULT 43
JN0250
dehydroshikimate dehydratase (EC 4.2.1.1) - Emeritella nidulans
C:Species: Emeritella nidulans, Aspergillus nidulans
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 12-Jul-2004
C:Accession: JN0250
R:Lamb, H.K.; Roberts, C.F.; Hawkins, A.R.
Gene 112, 219-224, 1992
A:Title: A second gene (guth) within the Aspergillus nidulans-quinic-acid utilisation 9
A:Reference number: JN0250; MUID:92210002; PMID:1339361
A:Accession: JN0250
A:Molecule type: mRNA
A:Residues: 1-348 <LAM>
A:Cross-references: UNIPROT:Q00774; UNIPARC:UPI000006A040; GB:M77665; NID:G3849800; PID
A:Note: the authors translated the codon ATA for residue 109 as Leu and GGG for residue
C:Genetics:
A:Gene: guth
C:Superfamily: 3-dehydroshikimate dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase; zinc
F:181-213/Region: zinc binding

Query Match 44.4%; Score 39.5; DB 2; Length 348;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 1 WEVLCW-----TWE 9
: | | | | |
159 YEALCWSHTVDIWE 172

Db

RESULT 44
D75195
hypothetical protein PAB2287 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75195
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: D75195
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-551 <KAW>
A:Cross-references: UNIPROT:Q9V2I7; UNIPARC:UPI000006322D; GB:AJ248283; GB:AL096836; NI
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2287
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB2287

Query Match 44.4%; Score 39.5; DB 2; Length 551;
Best Local Similarity 46.7%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 WEVLCW---WETCE 12
| | | | |
271 WTMLAWTSSKWTLE 285

Db

RESULT 45
AC3330
hypothetical protein BMEI0625 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AC3330
 R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AC3330
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-93 <KUR>
 A:Cross-references: UNIPROT:Q8YI20; UNIPROT:Q8FZU2; UNIPARC:UPI0000057D5B; GB:AE008917;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0625
 A:Map position: 1

Query Match 43.8%; Score 39; DB 2; Length 93;
 Best Local Similarity 83.3%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VLCWTW 8
 |||||
 Db 55 VLCWVW 60

RESULT 46
 C95847
 Hypothetical transmembrane protein SMB20040 [imported] - *Sinorhizobium meliloti* (strain
 C:Species: *Sinorhizobium meliloti*
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: C95847
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C95847
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <KUR>
 A:Cross-references: UNIPROT:Q92XB9; UNIPARC:UPI000004784; GB:AL591985; PIDN:CAC48443.1;
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R.; Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, H.; Hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMB20040
 A:Genome: plasmid

Query Match 43.8%; Score 39; DB 2; Length 286;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLWCW 6
 |||||
 Db 177 WQVICW 182

RESULT 47
 AE3273
 transporter, dme family BMEI0170 [imported] - *Brucella melitensis* (strain 16M)
 C:Species: *Brucella melitensis*
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AE3273
 R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AE3273
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-301 <KUR>
 A:Cross-references: UNIPROT:Q8YJB6; UNIPARC:UPI0000057B97; GB:AE008917; PIDN:AA51352.1;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0170
 A:Map position: 1

Query Match 43.8%; Score 39; DB 2; Length 301;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEVLWCW 6
 |||||
 Db 192 WQVICW 197

RESULT 48
 T49995
 cyclin protein-like - *Arabidopsis thaliana*
 N:Alternate names: protein F12B17.210
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T49995
 R:Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25026
 A:Accession: T49995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <BEV>
 A:Cross-references: UNIPROT:Q9LX96; UNIPARC:UPI000009D855; EMBL:AL353995; GSPDB:GN00063.
 A:Experimental source: cultivar Columbia; BAC clone F12B17
 C:Genetics:
 A:Gene: ARSP:F12B17.210
 A:Map position: 5
 A:Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match 43.8%; Score 39; DB 2; Length 317;
 Best Local Similarity 45.5%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EYLCWTWTCCE 12
 |||||
 Db 71 QALGWIWKACE 81

RESULT 49
 AB3597
 galactoside transport system permease protein mgIC [imported] - *Brucella melitensis* (st)
 C:Species: *Brucella melitensis*
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C:Accession: AB3597
 R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, M.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AB3597
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-333 <KUR>
 A:Cross-references: UNIPROT:Q8YC33; UNIPARC:UPI00000585AA; GB:AE008918; PIDN:AA513941.1
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0699
 A:Map position: II

Query Match 43.8%; Score 39; DB 2; Length 333;

Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWTET 10
| | | | |
DB 302 WRALCWRFT 311

RESULT 50
JC7695
G protein-coupled receptor, SLT receptor - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: JC7695
R;Mori, M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shind
Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001
A;Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-co
A;Reference number: JC7695; MUID:21255282; PMID:11355873
A;Contents: Hippocampus
A;Accession: JC7695
A;Molecule type: mRNA
A;Residues: 1-340 <MOR>
A;Cross-references: UNIPROT:Q969V1; UNIPARC:UPI000003730F; DBJ:AB060151
C;Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re
memory.
C;Genetics:
A;Gene: slt
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 43.8%; Score 39; DB 2; Length 340;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLCWTWE 9
| | | | |
DB 220 ILCYTWE 226

Search completed: March 28, 2006, 11:51:32
Job time : 55 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:43:34 ; Search time 235 Seconds
(without alignments)
39.029 Million cell updates/sec

Title: US-10-639-076-4

Perfect score: 89

Sequence: 1 WEVLCTWETCER 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	64.0	306	2 Q55VS7	CRYNE
2	57	64.0	331	2 Q4PAW3	USTMA
3	52	58.4	1858	2 Q91PR6	9COMO
4	51	57.3	260	2 Q6CAB0	YARLI
5	51	57.3	292	2 Q4WEX3	ASPFU
6	51	57.3	292	2 Q05533	YEAST
7	51	57.3	295	2 Q6FSE7	CANGA
8	51	57.3	297	2 Q4ILE1	GIRZE
9	50	56.2	269	2 Q4SKD7	TETNG
10	50	56.2	567	2 Q5BLJ1	EMENI
11	49	55.1	395	2 Q9C693	ARATH
12	49	55.1	533	2 Q8RY80	ARATH
13	48	53.9	460	2 Q8C8K5	MOUSE
14	47	52.8	138	2 Q8CAZ0	MOUSE
15	47	52.8	236	2 P79899	ONCMY
16	47	52.8	236	2 P79905	SALSA
17	47	52.8	1026	2 Q7SZU5	NEUCR
18	46	51.7	137	2 Q4S5E2	TETNG
19	46	51.7	173	2 Q8OLJ0	NPVNC
20	46	51.7	175	2 Q8JMB3	9NUCL
21	46	51.7	232	2 Q71AG8	9NUCL
22	46	51.7	232	2 Q5UPF0	MIMIV
23	46	51.7	274	2 Q4XIV6	ASPFU
24	46	51.7	315	2 Q7B3G3	CLOTR
25	46	51.7	427	2 Q74498	SCHPO
26	46	51.7	564	2 Q4WQ46	ASPFU
27	46	51.7	1042	2 Q9GRV9	CABEL
28	46	51.7	1080	2 Q01979	CABEL
29	46	51.7	1085	2 Q6QJ35	CAEBR
30	46	51.7	1121	2 Q02252	CABEL
31	46	51.7	1230	2 Q59325	CLOTR

32	45.5	51.1	807	2	Q86P30	DROME
33	45.5	51.1	807	2	Q9V995	DROME
34	45	50.6	126	2	Q8N8D9	HUMAN
35	45	50.6	426	2	Q87830	STRAT
36	45	50.6	481	2	Q5ENM8	BRARE
37	45	50.6	513	2	Q4Q987	LEIMA
38	45	50.6	514	2	Q4WLK9	ASPFU
39	45	50.6	673	2	Q5L1D4	GEOKA
40	45	50.6	674	2	Q8A222	BACTN
41	45	50.6	895	2	Q68438	CLOTR
42	44	49.4	59	2	Q5R549	PONPY
43	44	49.4	155	2	Q8TNM4	METAC
44	44	49.4	168	2	Q9DFQ6	GILMI
45	44	49.4	240	2	Q5B307	EMENI
46	44	49.4	272	2	Q4HWV6	GIRZE
47	44	49.4	320	2	Q7YRB2	CANBF
48	44	49.4	350	2	Q8TVT5	METKA
49	44	49.4	360	2	Q6OVV2	CAEBR
50	44	49.4	421	2	Q57XP3	9TRYP
51	44	49.4	2030	2	Q4S3E8	TETNG
52	43.5	48.9	239	2	Q6G6F7	BURTH
53	43.5	48.9	239	2	Q62BG7	BURMA
54	43.5	48.9	239	2	Q6UBQ1	BURPS
55	43	48.3	187	2	Q850L0	9EUKA
56	43	48.3	205	2	Q96T57	HUMAN
57	43	48.3	339	2	Q611S0	CAEBR
58	43	48.3	361	1	ALR	CORGL
59	43	48.3	394	2	Q8TIA3	TRYCR
60	43	48.3	516	2	Q42701	CATRO
61	43	48.3	524	1	C72A1	CATRO
62	43	48.3	524	2	Q42700	CATRO
63	43	48.3	536	1	KCNN1	RAT
64	43	48.3	537	2	Q6JXY1	MOUSE
65	43	48.3	538	2	Q5CZY7	MOUSE
66	43	48.3	560	2	Q4W9T5	ASPFU
67	43	48.3	570	2	Q58FL1	ASPNG
68	43	48.3	580	1	KCNN1	MOUSE
69	43	48.3	605	2	Q7SAU4	NEUCR
70	43	48.3	605	2	Q6DE64	XENLA
71	43	48.3	1202	2	Q7Q7F2	ANOCA
72	43	48.3	1443	2	Q4T8K2	TETNG
73	42.5	47.8	88	2	Q8L6X3	BETCO
74	42.5	47.8	239	2	Q93NN8	BURML
75	42.5	47.8	239	2	Q93PF4	BURVI
76	42.5	47.8	239	2	Q93PF6	9BURK
77	42.5	47.8	239	2	Q93PF7	BURML
78	42.5	47.8	239	2	Q93PF9	BURCE
79	42.5	47.8	239	2	Q9AM46	BURCE
80	42.5	47.8	239	2	Q9AM47	BURVI
81	42.5	47.8	239	2	Q9AM48	9BURK
82	42.5	47.8	239	2	Q9AM49	BURCE
83	42.5	47.8	239	2	Q9AM50	BURML
84	42.5	47.8	239	2	Q9AM51	BURCE
85	42.5	47.8	239	2	Q9ZIU0	BURCE
86	42.5	47.8	239	2	Q4LVG7	9BURK
87	42.5	47.8	450	2	Q8K0H9	MOUSE
88	42.5	47.8	591	2	Q6FKE4	CANGA
89	42.5	47.8	844	2	Q7TSG3	MOUSE
90	42.5	47.8	1405	1	CRUM1	MOUSE
91	42	47.2	81	2	Q6LRR3	PROPR
92	42	47.2	103	2	Q5FW50	MOUSE
93	42	47.2	111	2	Q4WMB9	ASPFU
94	42	47.2	167	2	Q8BXG2	MOUSE
95	42	47.2	214	2	Q4Y1N0	PLACH
96	42	47.2	214	2	Q4Z402	PLABE
97	42	47.2	245	2	Q7SNE5	BOVIN
98	42	47.2	253	2	Q67R33	SYMTH
99	42	47.2	268	2	Q7NCX5	GLOVI
100	42	47.2	325	2	Q6D712	FRWCT
101	42	47.2	333	2	Q8ZVD3	HUMAN
102	42	47.2	347	2	Q29274	ARCFA
103	42	47.2	358	2	Q9SBS0	MEDVA
104	42	47.2	418	2	Q86VF9	HUMAN

Q86P30	drosophila
Q9V995	drosophila
Q8N8D9	homo sapien
Q87830	streptomyce
Q5ENM8	brachydanio
Q4Q987	leishmania
Q4WLK9	aspergillus
Q5L1D4	geobacillus
Q8A222	bacteroides
Q68438	clostridium
Q5R549	pongo pygma
Q8TNM4	methanosarc
Q9DFQ6	gilllichthys
Q5B307	aspergillus
Q4HWV6	gibberella
Q7YRB2	candidatus
Q8TVT5	methanopyru
Q6OVV2	caenorhabdi
Q57XP3	trypanosoma
Q4S3E8	tetradodon n
Q6G6F7	burkholderi
Q62BG7	burkholderi
Q6UBQ1	burkholderi
Q850L0	pseudosoch
Q96T57	homo sapien
Q611S0	caenorhabdi
Q8TIA3	corynebacte
Q42701	trypanosoma
Q05047	catharanthu
Q42700	catharanthu
P70606	rattus norv
Q6JXY1	mus musculu
Q5CZY7	mus musculu
Q4W9T5	aspergillus
Q58FL1	aspergillus
Q9EIR3	mus musculu
Q7SAU4	neurospora
Q6DE64	xenopus lae
Q7Q7F2	anopheles g
Q4T8K2	tetradodon n
Q8L6X3	beta coroll
Q93NN8	burkholderi
Q93PF4	burkholderi
Q93PF6	burkholderi
Q93PF7	burkholderi
Q93PF9	burkholderi
Q9AM46	burkholderi
Q9AM47	burkholderi
Q9AM48	burkholderi
Q9AM49	burkholderi
Q9AM50	burkholderi
Q9AM51	burkholderi
Q9ZIU0	burkholderi
Q4LVG7	burkholderi
Q8K0H9	mus musculu
Q6FKE4	candida gla
Q7TSG3	mus musculu
Q8VNS2	mus musculu
Q6LRR3	photobacter
Q5FW50	mus musculu
Q4WMB9	aspergillus
Q8BXG2	mus musculu
Q4Y1N0	plasmodium
Q4Z402	plasmodium
Q7SNE5	bos taurus
Q67R33	symbiobacte
Q7NCX5	gloeobacter
Q6D712	erwinia car
Q8ZVD3	homo sapien
Q29274	archaeoglob
Q9SBS0	medicago va
Q86VF9	homo sapien

105	42	47.2	426	2	Q8XKG7 HUMAN	Q8XKG7 homo sapien	178	41	46.1	330	1	QUTG_EMENI	P25416 emericella
106	42	47.2	432	2	Q8XK11_MOUSE	Q8XK11 mus musculus	179	41	46.1	330	2	Q4WSU4 ASPFU	Q4wsu4 aspergillus
107	42	47.2	439	2	Q8BPH2_MOUSE	Q8BPH2 mus musculus	180	41	46.1	331	2	Q6MYX4 ASPFU	Q6myx4 aspergillus
108	42	47.2	444	2	Q4SFG2_TETNG	Q4SFG2 tetraodon n	181	41	46.1	335	2	Q86ZM2_PODAN	Q86zm2 podospora a
109	42	47.2	475	2	Q4SFG2_TETNG	Q4SFG2 tetraodon n	182	41	46.1	335	2	Q86ZM2_PODAN	P11634 neurospora
110	42	47.2	478	2	Q4QFB9_LEITHA	Q4QFB9 leishmania	183	41	46.1	352	2	Q51XV2_MAGGR	Q51xv2 magnaporthe
111	42	47.2	501	2	Q9SVJ6_ARATH	Q9SVJ6 arabidopsis	184	41	46.1	361	2	Q6M9Z6_PAGUR	Q6m9z6 parachlamy
112	42	47.2	502	2	Q93WC5_ARATH	Q93WC5 arabidopsis	185	41	46.1	371	2	Q6FDF3_ACIAD	Q6fdf3 acinetobact
113	42	47.2	514	2	Q52AI7_MAGGR	Q52AI7 magnaporthe	186	41	46.1	388	2	Q41205_GIBZE	Q412q5 gibberella
114	42	47.2	515	2	Q4SBN1_TETNG	Q4SBN1 tetraodon n	187	41	46.1	397	2	Q7WAI2_BORPA	Q7wai2 bordetella
115	42	47.2	542	2	Q5KR10_HUMAN	Q5KR10 homo sapien	188	41	46.1	397	2	Q7WJMG_BORBR	Q7wjmg bordetella
116	42	47.2	543	2	Q6DJU4_HUMAN	Q6DJU4 homo sapien	189	41	46.1	416	1	PXN1_XENLA	P49263 xenopus lae
117	42	47.2	545	2	Q90ZP5_ONCMY	Q90ZP5 oncorhynch	190	41	46.1	437	2	Q91TM5_TUVV1	Q91tms tupaiid her
118	42	47.2	553	2	Q9PFS9_CHICK	Q9PFS9 gallus gall	191	41	46.1	449	2	Q96UK4_COCIM	Q96uk4 coccidioid
119	42	47.2	561	1	Q8KNN1_HUMAN	Q8KNN1 homo sapien	192	41	46.1	481	2	Q33088_MYCLE	Q33088 mycobacteri
120	42	47.2	564	1	Q8CF73_MOUSE	Q8CF73 mus musculus	193	41	46.1	494	2	Q21652_CABEL	Q21652 caenorhabdi
121	42	47.2	569	1	UREI_STNY3	P73061 synectocyt	194	41	46.1	496	2	Q61UP6_CABBR	Q61up6 caenorhabdi
122	42	47.2	574	1	Q540U5_MOUSE	P58390 mus musculus	195	41	46.1	497	2	Q75KY5_ORYSA	Q75ky5 oryza sativ
123	42	47.2	574	1	Q540U5_MOUSE	Q540u5 mus musculus	196	41	46.1	502	2	Q688G5_ORYSA	Q688g5 oryza sativ
124	42	47.2	579	1	Q8XK21_MOUSE	Q8XK21 homo sapien	197	41	46.1	519	2	Q81RR8_DROME	Q81rr8 drosophila
125	42	47.2	580	1	Q8XK21_MOUSE	Q8XK21 homo sapien	198	41	46.1	522	2	Q8MRM1_DROME	Q8mrml drosophila
126	42	47.2	580	1	Q8XK21_MOUSE	Q8XK21 homo sapien	199	41	46.1	530	2	Q6EPA9_ORYSA	Q6epa9 oryza sativ
127	42	47.2	581	2	Q766U8_BOVIN	P70804 rattus norv	200	41	46.1	559	2	Q6NLO3_ARATH	Q6nlo3 arabidopsis
128	42	47.2	584	2	Q766U7_BOVIN	Q766u7 bos taurus	201	41	46.1	563	2	Q6ZNL4_HUMAN	Q6znl4 homo sapien
129	42	47.2	628	2	Q7S409_NEUCR	Q7S409 neurospora	202	41	46.1	572	2	Q7Q8X2_ANOGA	Q7q8x2 anopheles g
130	42	47.2	649	2	Q8CAD4_MOUSE	Q8CAD4 mus musculus	203	41	46.1	573	2	Q9W4C6_DROME	Q9w4c6 drosophila
131	42	47.2	709	2	Q4SU70_TETNG	Q4SU70 tetraodon n	204	41	46.1	575	2	Q9C9A7_ARATH	Q9c9a7 arabidopsis
132	42	47.2	716	2	Q948Z6_SOLTU	Q948z6 solanum tub	205	41	46.1	594	2	Q83287_TREPA	Q83287 treponema p
133	42	47.2	724	1	Q8KNN3_PIG	P58392 sus scrofa	206	41	46.1	608	2	Q8NFZ6_CORDI	Q8nfz6 corynebacte
134	42	47.2	731	1	Q8KNN3_MOUSE	P58391 mus musculus	207	41	46.1	615	2	Q79VE0_CORGL	Q79ve0 corynebacte
135	42	47.2	731	2	Q5VT74_HUMAN	Q5VT74 homo sapien	208	41	46.1	615	2	Q8FNC7_COREF	Q8fnc7 corynebacte
136	42	47.2	732	1	Q8KNN3_EAT	P70805 rattus norv	209	41	46.1	623	2	Q4CJW1_CORJK	Q4cjw1 corynebacte
137	42	47.2	736	1	Q8KNN3_HUMAN	Q8KNN3 homo sapien	210	41	46.1	651	2	Q9C9S7_ARATH	Q9c9s7 arabidopsis
138	42	47.2	737	1	Q8KNN3_HUMAN	Q8KNN3 homo sapien	211	41	46.1	678	2	Q8BLF3_MOUSE	Q8blf3 mus musculus
139	42	47.2	737	2	Q6XJY2_HUMAN	Q6XJY2 homo sapien	212	41	46.1	695	2	Q7XNM7_ORYSA	Q7xnm7 oryza sativ
140	42	47.2	752	2	Q90ZP4_ONCMY	Q90ZP4 oncorhynch	213	41	46.1	706	2	Q8XZ11_RALSO	Q8xz11 ralatonia s
141	42	47.2	834	2	Q93X18_SOLTU	Q93X18 solanum tub	214	41	46.1	732	2	Q6G81_YERPS	Q6g81 yerainia ps
142	42	47.2	834	2	Q8CCH4_MOUSE	Q8CCH4 mus musculus	215	41	46.1	732	2	Q8ZJY1_YERPE	Q8zjy1 yerainia pe
143	42	47.2	841	2	Q8CCH4_MOUSE	Q8CCH4 mus musculus	216	41	46.1	753	2	Q4ZPS6_PSESY	Q4zps6 pseudomonas
144	42	47.2	893	2	Q613J2_CABER	Q613j2 caenorhabdi	217	41	46.1	791	1	WSCK_DROME	P83097 drosophila
145	42	47.2	1548	2	Q57TU4_9TRYP	Q57tu4 trypanosoma	218	41	46.1	809	2	Q9W4C7_DROME	Q9w4c7 drosophila
146	42	47.2	1598	2	Q4RIC7_TETNG	Q4ric7 tetraodon n	219	41	46.1	850	2	Q5BF08_EMENI	Q5bf08 aspergillus
147	41.5	46.6	355	2	Q8HZN6_PONPY	Q8hzn6 pongo pygma	220	41	46.1	856	2	Q9SYM1_ARATH	Q9sym1 arabidopsis
148	41.5	46.6	359	1	3SHD_NEUCR	P70746 neurospora	221	41	46.1	860	2	Q4WRS0_ASPFU	Q4wrs0 aspergillus
149	41.5	46.6	433	2	Q41534_GIBZE	Q41534 gibberella	222	41	46.1	868	2	Q7MZR7_PHOLL	Q7mzr7 photorhabdu
150	41.5	46.6	505	1	SS_PROPR	Q704c7 propionibac	223	41	46.1	924	2	Q7KWS5_DROME	Q7kw5 drosophila
151	41	46.1	115	2	Q6MYD8_ASPFU	Q6myd8 aspergillus	224	41	46.1	924	2	Q7KWS5_DROME	Q7kw5 drosophila
152	41	46.1	117	2	Q61VD7_9ECHO	Q61vd7 strongyloce	225	41	46.1	951	2	Q86TH1_HUMAN	Q86th1 homo sapien
153	41	46.1	129	2	Q656W8_ORYSA	Q656w8 oryza sativ	226	41	46.1	1031	2	Q6Q345_HUMAN	Q6q345 homo sapien
154	41	46.1	141	2	Q5DBK2_SCHJA	Q5dbk2 schistosoma	227	41	46.1	1085	2	Q9KNE5_VIBCH	Q9kne5 vibrio chol
155	41	46.1	179	2	Q7PNS9_ANOGA	Q7pns9 anopheles g	228	41	46.1	1146	2	Q8B2T7_PSESM	Q8b2t7 pseudomonas
156	41	46.1	200	2	SOLR1_RALSO	Q6za92 oryza sativ	229	41	46.1	1514	2	Q7XNR4_ORYSA	Q7xnr4 oryza sativ
157	41	46.1	236	1	SOLR1_RALSO	P58590 ralatonia s	230	41	46.1	1691	2	Q45409_CABEL	Q45409 caenorhabdi
158	41	46.1	236	1	SOLR2_RALSO	Q5919 ralatonia s	231	41	46.1	1693	2	Q95ZU8_CABEL	Q95zu8 caenorhabdi
159	41	46.1	238	2	Q4WAP5_ASPFU	Q4wap5 aspergillus	232	41	46.1	2038	2	Q4P370_USTMA	Q4p370 ustilago ma
160	41	46.1	240	2	Q7F7EL_ORYSA	Q7f7el oryza sativ	233	41	46.1	2266	2	Q6BER5_CABEL	Q6ber5 caenorhabdi
161	41	46.1	241	2	Q9JBA4_9NUCL	Q9jba4 spodoptera	234	40.5	45.5	177	2	Q4THV7_TETNG	Q4thv7 tetraodon n
162	41	46.1	242	2	Q96136_PLAF7	Q96136 plasmodium	235	40.5	45.5	488	2	Q7SLP8_MACFA	Q7slp8 macaca faec
163	41	46.1	268	2	Q5WN89_CABER	Q5wn89 caenorhabdi	236	40.5	45.5	493	2	Q6NIM9_CORDI	Q6nim9 corynebacte
164	41	46.1	276	2	Q9MIL2_ARATH	Q9mil2 arabidopsis	237	40.5	45.5	497	2	Q6A690_PROAC	Q6a690 propionibac
165	41	46.1	278	1	RRP1_YEAST	P35178 saccharomyc	238	40.5	45.5	610	2	Q6BWU9_DEBHA	Q6bwu9 debaryomyce
166	41	46.1	285	2	Q81S29_DROME	Q81s29 drosophila	239	40.5	45.5	900	2	Q4T988_TETNG	Q4t988 tetraodon n
167	41	46.1	285	2	Q81S28_DROME	Q81s28 drosophila	240	40.5	45.5	999	2	Q8BR49_MOUSE	Q8br49 m mus muscu
168	41	46.1	294	2	Q72JK9_THET2	Q72jk9 thermus the	241	40.5	45.5	1256	2	Q9M297_ARATH	Q9m297 arabidopsis
169	41	46.1	294	2	Q5GJ86_THET2	Q5gj86 thermus the	242	40.5	45.5	2131	2	Q4T8J2_TETNG	Q4t8j2 tetraodon n
170	41	46.1	296	2	Q41A07_GIBZE	Q41a07 gibberella	243	40.5	45.5	4861	2	Q15751_HUMAN	Q15751 homo sapien
171	41	46.1	305	2	Q5NAB8_ORYSA	Q5nab8 oryza sativ	244	40	44.9	94	2	Q52850_ORYSA	Q52850 oryza sativ
172	41	46.1	306	2	Q9RNS5_DEIRA	Q9rns5 deinococcus	245	40	44.9	114	2	Q8CBN6_MOUSE	Q8cbn6 mus musculus
173	41	46.1	310	2	Q4K654_PSEFS	Q4k654 pseudomonas	246	40	44.9	128	2	Q6ZWD3_HUMAN	Q6zwd3 homo sapien
174	41	46.1	312	2	Q6BL69_DEBHA	Q6bl69 debaryomyce	247	40	44.9	140	2	Q6GE53_STAR	Q6ge51 staphylococ
175	41	46.1	315	2	Q5BE94_EMENI	Q5be94 aspergillus	248	40	44.9	140	2	Q609H6_METCA	Q609h6 methylococc
176	41	46.1	316	2	Q9AEF9_9BURK	Q9aef9 janthinobac	249	40	44.9	140	2	Q5DH4_STAAC	Q5dh4 staphylococ
177	41	46.1	323	2	Q9N4Y6_CABEL	Q9n4y6 caenorhabdi	250	40	44.9	154	2	Q98H58_RHILLO	Q98h58 rhizobium 1

251	40	44.9	220	2	QBL436	hordeum vul	QBL436	hordeum vul	324	40	44.9	1856	2	Q5K9Q2	CRYN	Q5K9Q2	cryptococcu	Q5K9Q2	cryptococcu
252	40	44.9	251	1	SFSA	PROVM	Q7v4t9	prochloroco	325	40	44.9	2291	2	Q55J99	CRYN	Q55J99	cryptococcu	Q55J99	cryptococcu
253	40	44.9	253	1	QBA618	BACTN	Q8a618	bacteroides	326	40	44.9	4396	2	Q5H9M6	BOVIN	Q5H9M6	boa taurus	Q5H9M6	boa taurus
254	40	44.9	254	1	QFSA	SYNFX	Q7u9k2	synecococc	327	40	44.9	4881	2	Q6TAB6	GBACT	Q6TAB6	symblont ba	Q6TAB6	symblont ba
255	40	44.9	258	2	QBAKX5	BRARE	Q8uX55	brachydanio	328	39.5	44.4	185	2	Q82EW4	STRAW	Q82EW4	streptomyc	Q82EW4	streptomyc
256	40	44.9	259	2	Q8SUG2	ENCUC	Q8SUG2	encephalito	329	39.5	44.4	239	2	Q7B6T8	BURPS	Q7B6T8	burkholderi	Q7B6T8	burkholderi
257	40	44.9	259	2	Q7VZU3	BORPE	Q7vzu3	borderetella	330	39.5	44.4	312	2	Q7TFU1	RHCME	Q7TFU1	theus cyto	Q7TFU1	theus cyto
258	40	44.9	259	2	Q7M567	BORPA	Q7m567	borderetella	331	39.5	44.4	340	2	Q4IFX9	GIBZE	Q4IFX9	gibberella	Q4IFX9	gibberella
259	40	44.9	259	2	Q7MCP7	BORBR	Q7mcp7	borderetella	332	39.5	44.4	348	2	Q00774	EMENI	Q00774	emericella	Q00774	emericella
260	40	44.9	265	2	Q8IUS6	HUMAN	Q8ius6	homo sapien	333	39.5	44.4	367	2	Q5BE90	EMENI	Q5BE90	aspergillus	Q5BE90	aspergillus
261	40	44.9	280	2	Q5YI23	NOCFA	Q5yI23	nocardia fa	334	39.5	44.4	367	2	Q86ZM4	PODAN	Q86ZM4	podospora a	Q86ZM4	podospora a
262	40	44.9	280	2	Q7TZ08	MYCBO	Q7tz08	mycobacteri	335	39.5	44.4	451	2	Q4SIK7	TETNG	Q4SIK7	tetradodon n	Q4SIK7	tetradodon n
263	40	44.9	280	2	Q33253	MYCTU	Q33253	mycobacteri	336	39.5	44.4	499	2	Q8FRF7	COREF	Q8FRF7	corynebacte	Q8FRF7	corynebacte
264	40	44.9	281	2	Q73YV1	MYCPA	Q73yV1	mycobacteri	337	39.5	44.4	551	2	Q9V217	PYRAB	Q9V217	pyrococcus	Q9V217	pyrococcus
265	40	44.9	282	2	Q6ZP99	SYMTH	Q6zP99	syntrophobacte	338	39.5	44.4	567	2	Q59LAS	CANAL	Q59LAS	candida alb	Q59LAS	candida alb
266	40	44.9	291	2	Q6NZ03	BRARE	Q6nz03	brachydanio	339	39.5	44.4	1080	2	Q5BEH6	EMENI	Q5BEH6	aspergillus	Q5BEH6	aspergillus
267	40	44.9	294	2	Q6FPW9	CANGA	Q6fPw9	candida gla	340	39	43.8	55	2	Q83XD2	9CHLR	Q83XD2	roseiflexus	Q83XD2	roseiflexus
268	40	44.9	295	1	QAP12	HUMAN	Q8ixf9	homo sapien	341	39	43.8	71	2	Q5U7H2	DIGPU	Q5U7H2	digitallis p	Q5U7H2	digitallis p
269	40	44.9	295	1	YHK6	YEAST	Q38710	saccharomyc	342	39	43.8	93	2	Q57CC8	BRUAB	Q57CC8	bruceella ab	Q57CC8	bruceella ab
270	40	44.9	299	2	Q82LE1	STRAW	Q82le1	streptomyc	343	39	43.8	93	2	Q8FZU2	BRUSU	Q8FZU2	bruceella su	Q8FZU2	bruceella su
271	40	44.9	305	1	MRGA2	MOUSE	Q91w44	mus musculu	344	39	43.8	93	2	Q8YI20	BRUME	Q8YI20	bruceella me	Q8YI20	bruceella me
272	40	44.9	306	2	Q9A618	CAUCR	Q9a618	caulobacter	345	39	43.8	138	2	Q5AF42	CANAL	Q5AF42	candida alb	Q5AF42	candida alb
273	40	44.9	312	2	Q8TGG3	ASPFU	Q8tGg3	aspergillus	346	39	43.8	138	2	Q5AFS9	CANAL	Q5AFS9	candida alb	Q5AFS9	candida alb
274	40	44.9	312	2	Q4WSN2	ASPFU	Q4wsn2	aspergillus	347	39	43.8	155	2	Q9LOE6	STRCO	Q9LOE6	streptomyc	Q9LOE6	streptomyc
275	40	44.9	317	2	Q69UD6	ORYSA	Q69ud6	oryza sativ	348	39	43.8	181	2	Q4TAF5	TETNG	Q4TAF5	tetradodon n	Q4TAF5	tetradodon n
276	40	44.9	321	2	Q7V8P6	PROVM	Q7v8p6	prochloroco	349	39	43.8	185	2	Q985U6	RHILO	Q985U6	rhizobium l	Q985U6	rhizobium l
277	40	44.9	323	2	Q4I587	GIBZE	Q4i587	gibberella	350	39	43.8	189	2	Q6Z8B9	HUMAN	Q6Z8B9	homo sapien	Q6Z8B9	homo sapien
278	40	44.9	327	2	Q6U445	ORYSA	Q6u445	oryza sativ	351	39	43.8	189	2	Q6Z8B7	HUMAN	Q6Z8B7	homo sapien	Q6Z8B7	homo sapien
279	40	44.9	336	2	Q61C41	CAEBR	Q61c41	caenorhabdi	352	39	43.8	195	2	Q96H61	HUMAN	Q96H61	homo sapien	Q96H61	homo sapien
280	40	44.9	340	2	Q9MAG5	ARATH	Q9mag5	arabidopsis	353	39	43.8	206	2	Q82E45	STRAW	Q82E45	streptomyc	Q82E45	streptomyc
281	40	44.9	393	2	Q51UD0	MAGGR	Q51ud0	magnaporthe	354	39	43.8	213	2	Q6YX51	ORYSA	Q6YX51	oryza sativ	Q6YX51	oryza sativ
282	40	44.9	393	2	Q67R50	SYMTH	Q67r50	syntrophobacte	355	39	43.8	216	2	Q8D8V6	VIBVU	Q8D8V6	vibriu vuln	Q8D8V6	vibriu vuln
283	40	44.9	394	2	Q4QH80	LEIMA	Q4qh80	leishmania	356	39	43.8	216	2	Q7MLL8	VIBVU	Q7MLL8	vibriu vuln	Q7MLL8	vibriu vuln
284	40	44.9	415	2	Q9P519	NEUCR	Q9p519	neurospora	357	39	43.8	236	2	Q589R6	CIOIN	Q589R6	ciona intes	Q589R6	ciona intes
285	40	44.9	416	2	Q04507	ARATH	Q04507	arabidopsis	358	39	43.8	236	2	Q7XRR0	ORYSA	Q7XRR0	oryza sativ	Q7XRR0	oryza sativ
286	40	44.9	423	2	Q4WEY3	ASPFU	Q4wey3	aspergillus	359	39	43.8	238	2	P89905	SIVCZ	P89905	chimpanzee	P89905	chimpanzee
287	40	44.9	428	2	Q4IMW4	GIBZE	Q4imw4	gibberella	360	39	43.8	252	2	Q7P0P4	CHRVU	Q7P0P4	chromobacte	Q7P0P4	chromobacte
288	40	44.9	437	2	Q93XC2	ARATH	Q93xc2	arabidopsis	361	39	43.8	255	2	Q8IDK2	PLAF7	Q8IDK2	plasmodium	Q8IDK2	plasmodium
289	40	44.9	443	2	Q5ZCD6	ORYSA	Q5zcd6	oryza sativ	362	39	43.8	261	2	Q8N8W3	HUMAN	Q8N8W3	homo sapien	Q8N8W3	homo sapien
290	40	44.9	444	2	Q6W653	ORYSA	Q6w653	oryza sativ	363	39	43.8	268	2	Q95616	HUMAN	Q95616	homo sapien	Q95616	homo sapien
291	40	44.9	450	2	Q6LAX7	ORYSA	Q6lax7	oryza sativ	364	39	43.8	270	2	Q5LWE9	SILFO	Q5LWE9	silicibacte	Q5LWE9	silicibacte
292	40	44.9	471	2	Q4WM43	ASPFU	Q4wm43	aspergillus	365	39	43.8	285	2	Q8NDA7	HUMAN	Q8NDA7	homo sapien	Q8NDA7	homo sapien
293	40	44.9	491	2	Q9AXH3	LYCES	Q9axh3	lycopersico	366	39	43.8	285	2	Q57B02	BRUAB	Q57B02	bruceella ab	Q57B02	bruceella ab
294	40	44.9	515	2	Q4T374	TETNG	Q4t374	tetradodon n	367	39	43.8	285	2	Q8FYI1	BRUSU	Q8FYI1	bruceella su	Q8FYI1	bruceella su
295	40	44.9	579	2	Q6PPG3	CHLRE	Q6ppg3	chlamydomon	368	39	43.8	286	2	Q92XB9	RHIME	Q92XB9	rhizobium m	Q92XB9	rhizobium m
296	40	44.9	602	2	Q52DY6	MAGGR	Q52dy6	magnaporthe	369	39	43.8	289	2	Q50NK3	ENTHI	Q50NK3	entamoeba h	Q50NK3	entamoeba h
297	40	44.9	613	2	Q4S098	TETNG	Q4s098	tetradodon n	370	39	43.8	290	1	AQPI12	MOUSE	AQPI12	mus musculu	AQPI12	mus musculu
298	40	44.9	614	2	Q18656	CABEL	Q18656	caenorhabdi	371	39	43.8	290	2	Q76LB4	PAROL	Q76LB4	paralichthy	Q76LB4	paralichthy
299	40	44.9	738	2	Q4QAP6	LEIMA	Q4qap6	leishmania	372	39	43.8	291	2	Q6FB38	ACIAD	Q6FB38	acinobact	Q6FB38	acinobact
300	40	44.9	741	1	TLE4	RAT	Q07141	rattus norv	373	39	43.8	291	2	Q98L83	RHILO	Q98L83	rhizobium l	Q98L83	rhizobium l
301	40	44.9	782	2	Q4T6K8	TETNG	Q4t6k8	tetradodon n	374	39	43.8	298	2	Q6NKU1	ARATH	Q6NKU1	arabidopsis	Q6NKU1	arabidopsis
302	40	44.9	801	2	Q4T2D9	TETNG	Q4t2d9	tetradodon n	375	39	43.8	301	2	Q8YJB6	BRUME	Q8YJB6	bruceella me	Q8YJB6	bruceella me
303	40	44.9	804	1	PHK	MYCPA	Q73zm8	mycobacteri	376	39	43.8	302	2	Q50MX6	ENTHI	Q50MX6	entamoeba h	Q50MX6	entamoeba h
304	40	44.9	811	2	Q95U94	9NEOP	Q95u94	namestia co	377	39	43.8	302	2	Q4M003	9BURK	Q4M003	burkholderi	Q4M003	burkholderi
305	40	44.9	817	2	Q8R2S8	MOUSE	Q8r2s8	mus musculu	378	39	43.8	302	2	Q63W10	BURPS	Q63W10	burkholderi	Q63W10	burkholderi
306	40	44.9	819	2	Q9YHCl	PERVU	Q9yhcl	perca flave	379	39	43.8	302	2	Q621C7	BURMA	Q621C7	burkholderi	Q621C7	burkholderi
307	40	44.9	828	2	Q4RG88	TETNG	Q4rg88	tetradodon n	380	39	43.8	304	2	Q4KGZ7	PSSEF	Q4KGZ7	pseudomonas	Q4KGZ7	pseudomonas
308	40	44.9	855	2	P91175	CABEL	P91175	caenorhabdi	381	39	43.8	308	2	Q8LGA1	ARATH	Q8LGA1	arabidopsis	Q8LGA1	arabidopsis
309	40	44.9	871	2	Q4SKW9	TETNG	Q4skw9	tetradodon n	382	39	43.8	308	2	Q9XFR7	ARATH	Q9XFR7	arabidopsis	Q9XFR7	arabidopsis
310	40	44.9	885	2	Q6PFT2	BRARE	Q6pft2	brachydanio	383	39	43.8	308	2	Q9XFR7	ARATH	Q9XFR7	arabidopsis	Q9XFR7	arabidopsis
311	40	44.9	888	2	Q4RZW9	TETNG	Q4rzw9	tetradodon n	384	39	43.8	313	2	Q7UMC2	RHQB	Q7UMC2	rhodopirell	Q7UMC2	rhodopirell
312	40	44.9	895	2	Q9W6N1	PERVU	Q9w6n1	perca flave	385	39	43.8	314	2	Q4IHT1	GIBZE	Q4IHT1	gibberella	Q4IHT1	gibberella
313	40	44.9	916	2	Q4RTN2	TETNG	Q4rtn2	tetradodon n	386	39	43.8	314	2	Q6J1Z6	COMTE	Q6J1Z6	comonomas t	Q6J1Z6	comonomas t
314	40	44.9	945	2	Q6C850	YARLI	Q6c850	yarrowia li	387	39	43.8	317	2	Q9LX96	ARATH	Q9LX96	arabidopsis	Q9LX96	arabidopsis
315	40	44.9	1050	2	Q6GPV3	XENLA	Q6gpv3	xenopus lae	388	39	43.8	325	2	Q60VV3	CAEBR	Q60VV3	caenorhabdi	Q60VV3	caenorhabdi
316	40	44.9	1080	1	ADCV7	HUMAN	P51828	homo sapien	389	39	43.8	325	2	Q918C2	XENLA	Q918C2	xenopus lae	Q918C2	xenopus lae
317	40	44.9	1086	2	Q5ESH0	VIBF1	Q5esh0	vibriu fisc	390	39	43.8	326	2	Q4I5Q3	GIBZE	Q4I5Q3	gibberella	Q4I5Q3	gibberella
318	40	44.9	1126	2	Q500A3	PSSEY	Q500a3	pseudomonas	391	39	43.8	326	2	Q6F7N3	ACIAD	Q6F7N3	acinobact	Q6F7N3	acinobact
319	40	44.9	1132	2	Q4ZQ88	PSSEY	Q4zq88	pseudomonas	392	39	43.8	330	2	Q8M1P5	CANFA	Q8M1P5	canis fami	Q8M1P5	canis fami
320	40	44.9	1142	2	Q885D1	PSSEY	Q885d1	pseudomonas	393	39	43.8	333	2	Q940V2	ARATH	Q940V2	arabidopsis	Q940V2	arabidopsis
321	40	44.9	1209	2	Q7Q9V0</														

397	39	43.8	340	1	MCHR2_HUMAN	Q969v1	homo sapien	470	39	43.8	1253	2	Q9UN29_HUMAN	Q9UN29	homo sapien
398	39	43.8	340	1	MCHR22_MACFA	Q8q54	macaca fasc	471	39	43.8	1253	2	Q96F07_HUMAN	Q96F07	homo sapien
399	39	43.8	340	1	MCHR22_MACFA	Q8q54	macaca mufa	472	39	43.8	1253	2	Q7L576_HUMAN	Q7L576	homo sapien
400	39	43.8	340	2	Q8MIN7_MUSPU	Q8min7	homo sapien	473	39	43.8	1253	2	Q5R414_PONPY	Q5r414	pongo pygma
401	39	43.8	340	2	Q8MIN7_MUSPU	Q8min7	mustela put	474	39	43.8	1253	2	Q5R619_PONPY	Q5r619	pongo pygma
402	39	43.8	341	2	Q6LJL9_CABER	Q6llj9	caenorhabdi	475	39	43.8	1253	2	Q88558_MOUSE	Q88558	mus musculus
403	39	43.8	341	2	Q6LJL9_CABER	Q6llj9	caenorhabdi	476	39	43.8	1253	2	Q5SQX6_MOUSE	Q5sqx6	mus musculus
404	39	43.8	341	2	Q6LJL9_CABER	Q6llj9	caenorhabdi	477	39	43.8	1253	2	Q924D3_MOUSE	Q924d3	mus musculus
405	39	43.8	342	2	Q18733_CABEL	Q18733	caenorhabdi	478	39	43.8	1253	2	Q8BSW0_MOUSE	Q8bsw0	mus musculus
406	39	43.8	342	2	Q6H6Q6_ORISA	Q6h6q6	oryza sativ	479	39	43.8	1253	2	Q7TMB8_MOUSE	Q7tmb8	mus musculus
407	39	43.8	342	2	Q9R181_MOUSE	Q9r181	mus musculus	480	39	43.8	1253	2	Q6GQD1_YENLA	Q6gqd1	xenopus lae
408	39	43.8	343	2	Q983R9_RHILO	Q983r9	rhizobium l	481	39	43.8	1259	2	Q8CHA9_MOUSE	Q8cha9	mus musculus
409	39	43.8	343	2	Q7Y1H1_ORISA	Q7y1h1	oryza sativ	482	39	43.8	1262	2	Q80VN6_MOUSE	Q80vn6	mus musculus
410	39	43.8	344	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	483	39	43.8	1271	2	Q14467_HUMAN	Q14467	homo sapien
411	39	43.8	345	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	484	39	43.8	1279	2	Q5DU50_MOUSE	Q5du50	mus musculus
412	39	43.8	345	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	485	39	43.8	1280	2	Q7L2G3_ARATH	Q7l2g3	arabidopsis
413	39	43.8	345	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	486	39	43.8	1281	2	Q9ULQ2_HUMAN	Q9ulq2	homo sapien
414	39	43.8	345	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	487	39	43.8	1283	2	Q53ENS_HUMAN	Q53ens	homo sapien
415	39	43.8	345	2	Q6K7P6_ORISA	Q6k7p6	oryza sativ	488	39	43.8	1305	2	Q80560_ARATH	Q80560	arabidopsis
416	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	489	39	43.8	1319	2	Q4T9C5_TETNG	Q4t9c5	tetradodon n
417	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	490	39	43.8	1513	2	Q7SCN1_NEUCR	Q7scn1	neurospora
418	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	491	39	43.8	1607	1	MIPL_LYNSI	Q25410	l putative
419	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	492	39	43.8	1829	2	Q19815_CABEL	Q19815	caenorhabdi
420	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	493	39	43.8	1849	2	Q61KM2_CABER	Q61km2	caenorhabdi
421	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	494	39	43.8	2049	2	Q20849_CABEL	Q20849	caenorhabdi
422	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	495	39	43.8	2163	2	Q7Q328_ANOGA	Q7q328	anopheles g
423	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	496	39	43.8	2241	2	Q4SD94_TETNG	Q4sd94	tetradodon n
424	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	497	39	43.8	2524	2	Q50YB7_ENTHI	Q50yb7	entamoeba h
425	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	498	39	43.8	97	2	Q7QPM8_GIALA	Q7qpm8	giardia lam
426	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	499	39	43.8	121	2	Q6R5H3_MOUSE	Q6r5h3	mus musculus
427	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	500	39	43.8	168	2	Q4RMS3_TETNG	Q4rms3	tetradodon n
428	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	501	39	43.8	238	2	Q59GB9_HUMAN	Q59gb9	homo sapien
429	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	502	39	43.8	261	2	Q5KM17_CRYNE	Q5km17	cryptococcu
430	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	503	39	43.8	279	2	Q4I6L3_GIBZE	Q4i6l3	gibberella
431	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	504	39	43.8	434	2	Q7SC18_NEUCR	Q7sc18	neurospora
432	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	505	39	43.8	442	2	Q4WQ51_ASPFU	Q4wq51	aspergillus
433	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	506	39	43.8	446	2	Q6FRU2_CANGA	Q6fru2	candida gla
434	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	507	39	43.8	447	2	Q7SY25_XENLA	Q7sy25	xenopus lae
435	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	508	39	43.8	488	1	HDAC2_HUMAN	HDAC2	homo sapien
436	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	509	39	43.8	488	1	HDAC2_MOUSE	HDAC2	homo sapien
437	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	510	39	43.8	488	2	Q66J55_XENLA	Q66j55	xenopus tro
438	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	511	39	43.8	488	2	Q6GLI1_XENTR	Q6gli1	xenopus tro
439	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	512	39	43.8	540	2	Q4RX65_TETNG	Q4rx65	tetradodon n
440	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	513	39	43.8	540	2	Q51MB9_MAGGR	Q51me9	magnaporthe
441	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	514	39	43.8	555	2	Q4Q6E7_LEIMA	Q4q6e7	leishmania
442	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	515	39	43.8	629	2	Q4Q6E7_LEIMA	Q4q6e7	leishmania
443	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	516	39	43.8	665	2	Q55XX7_CRYNE	Q55xx7	cryptococcu
444	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	517	39	43.8	786	2	Q5W815_BRARE	Q5w815	brachydanio
445	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	518	39	43.8	1011	2	Q9SN80_ARATH	Q9sn80	arabidopsis
446	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	519	39	43.8	1036	2	Q4P8S1_USTMA	Q4p8s1	ustilago ma
447	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	520	39	43.8	2330	1	EGFL4_MOUSE	P60882	mus musculus
448	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	521	39	43.8	2386	1	EGFL4_MOUSE	P60882	mus musculus
449	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	522	39	43.8	69	2	Q68DR9_HUMAN	Q68dr9	homo sapien
450	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	523	39	43.8	71	2	Q95NH5_9DIPT	Q95nh5	drosophila
451	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	524	39	43.8	71	2	Q8IRD6_DROME	Q8ird6	drosophila
452	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	525	39	43.8	71	2	Q8IRD7_DROME	Q8ird7	drosophila
453	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	526	39	43.8	75	1	LCR75_ARATH	P82784	arabidopsis
454	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	527	39	43.8	78	2	Q6ILK0_DROME	Q6ilk0	drosophila
455	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	528	39	43.8	89	2	Q5PAL6_ANAMM	Q5pal6	anaplasmia m
456	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	529	39	43.8	90	2	Q4KWL5_NAIZE	Q4kwl5	zea mays
457	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	530	39	43.8	90	2	Q4SNF5_TETNG	Q4snf5	tetradodon n
458	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	531	39	43.8	96	2	Q4FH06_SAMCR	Q4fh06	samia cynth
459	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	532	39	43.8	104	2	Q9UY28_PPRAB	Q9uy28	pyrococcus
460	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	533	39	43.8	111	2	Q95682_DAUCA	Q95682	daucus caro
461	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	534	39	43.8	112	2	Q5S659_MOUSE	Q5s659	mus musculus
462	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	535	39	43.8	116	2	Q8CC76_MOUSE	Q8cc76	mus musculus
463	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	536	39	43.8	117	2	Q9F817_CARHY	Q9f817	carboxydoth
464	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	537	39	43.8	122	2	Q7RUM3_NEUCR	Q7rum3	neurospora
465	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	538	39	43.8	127	2	Q8UB9_MOUSE	Q8ub9	mus musculus
466	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	539	39	43.8	123	2	Q4SRW3_TETNG	Q4srw3	tetradodon n
467	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	540	39	43.8	124	2	Q8MQY0_DROME	Q8mqy0	drosophila
468	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	541	39	43.8	129	2	Q8MQY0_DROME	Q8mqy0	drosophila
469	39	43.8	346	2	Q5R1U4_MAGGR	Q5r1u4	magnaporthe	542	39	43.8	153	2	Q7SSW5_SIVCZ	Q7ssw5	chimpanzee

543	38	42.7	155	2	Q8WZ04_HUMAN	Q8WZ04	homo sapien	616	38	42.7	215	1	VIF_HV2ST	P20878	human immun
544	38	42.7	158	2	Q67N43_SYNTH	Q67N43	symbolacte	617	38	42.7	215	2	Q51Q28_MAGGR	Q51Q28	magnaporthes
545	38	42.7	166	2	Q5V891_HALMA	Q5V891	haloarcula	618	38	42.7	215	2	Q9SA07_ARATH	Q9SA07	arabidopsis
546	38	42.7	179	2	Q61306_ORYSA	Q61306	oryza sativ	619	38	42.7	215	2	P88143_9HIV2	P88143	human immun
547	38	42.7	179	2	Q81268_ORYSA	Q81268	oryza sativ	620	38	42.7	215	2	Q6R783_9HIV2	Q6R783	human immun
548	38	42.7	179	2	Q8SX05_ORYSA	Q8SX05	oryza sativ	621	38	42.7	215	2	Q6R792_9HIV2	Q6R792	human immun
549	38	42.7	180	2	Q5OM16_ENTHI	Q5OM16	entamoeba h	622	38	42.7	215	2	Q76622_9HIV2	Q76622	human immun
550	38	42.7	180	2	Q5N797_ORYSA	Q5N797	oryza sativ	623	38	42.7	215	2	Q80635_9HIV2	Q80635	human immun
551	38	42.7	183	2	Q8V623_9GEMI	Q8V623	afriican cas	624	38	42.7	215	2	Q80636_9HIV2	Q80636	human immun
552	38	42.7	188	2	Q4PLY2_IXOSC	Q4PLY2	ixodes scap	625	38	42.7	215	2	Q80637_9HIV2	Q80637	human immun
553	38	42.7	199	2	Q41BW9_GIBZ	Q41BW9	giberella	626	38	42.7	215	2	Q91BL8_9HIV2	Q91BL8	human immun
554	38	42.7	200	2	Q677X7_9VIRU	Q677X7	lymphocysti	627	38	42.7	215	2	Q9VTT9_9HIV2	Q9VTT9	human immun
555	38	42.7	202	2	Q63XH5_BURPS	Q63XH5	burkholderi	628	38	42.7	216	1	VIF_HV2D2	P15834	human immun
556	38	42.7	206	2	Q5V834_HALMA	Q5V834	haloarcula	629	38	42.7	216	2	Q76635_9HIV2	Q76635	human immun
557	38	42.7	212	2	Q9BQ33_HUMAN	Q9BQ33	homo sapien	630	38	42.7	216	2	Q89753_9HIV2	Q89753	human immun
558	38	42.7	213	2	Q7X9H3_ARATH	Q7X9H3	arabidopsis	631	38	42.7	216	2	Q8UTV6_9HIV2	Q8UTV6	human immun
559	38	42.7	213	2	Q7SN86_SIVCZ	Q7SN86	chimpanzee	632	38	42.7	223	2	Q7SNM3_9HIV2	Q7SNM3	human immun
560	38	42.7	213	2	Q7SN87_SIVCZ	Q7SN87	chimpanzee	633	38	42.7	227	2	Q61VP1_CABBR	Q61VP1	caenorhabdi
561	38	42.7	213	2	Q7SN88_SIVCZ	Q7SN88	chimpanzee	634	38	42.7	229	1	VIF_CAEVC	P33462	caprine art
562	38	42.7	214	1	VIF_SIVM1	P05903	simian immu	635	38	42.7	229	2	Q56N28_CAEV	Q56N28	caprine art
563	38	42.7	214	1	VIF_SIVM2	P05902	simian immu	636	38	42.7	238	2	Q52A40_MAGGR	Q52A40	magnaporthes
564	38	42.7	214	1	VIF_SIVS4	P12505	simian immu	637	38	42.7	238	2	Q98NZ0_RHILO	Q98NZ0	rhizobium l
565	38	42.7	214	1	VIF_SIVSP	P19506	simian immu	638	38	42.7	241	2	Q4LQTO_9BURL	Q4LQTO	burkholderi
566	38	42.7	214	2	Q8VP39_ECOLI	Q8VP39	escherichia	639	38	42.7	242	2	Q74EF1_GEOSL	Q74EF1	geobacter s
567	38	42.7	214	2	Q11784_SIVCZ	O11784	chimpanzee	640	38	42.7	243	2	Q5E170_VIBF1	Q5E170	vibrio fisc
568	38	42.7	214	2	Q51060_SIVCZ	Q51060	chimpanzee	641	38	42.7	244	2	Q8VUR3_VIBPA	Q8VUR3	vibrio para
569	38	42.7	214	2	Q90318_SIVCZ	Q90318	chimpanzee	642	38	42.7	244	2	Q8RUX0_DEIRA	Q8RUX0	deinococcus
570	38	42.7	214	2	Q04249_SIVCZ	Q04249	chimpanzee	643	38	42.7	245	2	Q87H13_VIBPA	Q87H13	vibrio para
571	38	42.7	214	2	Q5QF18_SIVCZ	Q5QF18	chimpanzee	644	38	42.7	250	2	Q5OP12_ENTHI	Q5OP12	entamoeba h
572	38	42.7	214	2	Q5QFV5_SIVCZ	Q5QFV5	chimpanzee	645	38	42.7	251	2	Q8D4G2_VIBUO	Q8D4G2	vibrio vuln
573	38	42.7	214	2	Q5QFK7_SIVCZ	Q5QFK7	chimpanzee	646	38	42.7	254	2	Q6XN54_RHOOC	Q6XN54	rhodococcus
574	38	42.7	214	2	Q5QFL1_SIVCZ	Q5QFL1	chimpanzee	647	38	42.7	257	2	Q5OP13_ENTHI	Q5OP13	entamoeba h
575	38	42.7	214	2	Q5QFM2_SIVCZ	Q5QFM2	chimpanzee	648	38	42.7	258	2	Q8HIT2_GOSHI	Q8HIT2	gossypium h
576	38	42.7	214	2	Q5QFN3_SIVCZ	Q5QFN3	chimpanzee	649	38	42.7	262	1	DET2_ARATH	Q38944	arabidopsis
577	38	42.7	214	2	Q5QFR2_SIVCZ	Q5QFR2	chimpanzee	650	38	42.7	262	2	Q9XU29_CAEEL	Q9XU29	caenorhabdi
578	38	42.7	214	2	Q5QFS1_SIVCZ	Q5QFS1	chimpanzee	651	38	42.7	263	2	Q9FR36_SOYBN	Q9FR36	glycine max
579	38	42.7	214	2	Q5QFT2_SIVCZ	Q5QFT2	chimpanzee	652	38	42.7	265	2	Q5L2H1_GROKA	Q5L2H1	geobacillus
580	38	42.7	214	2	Q5QFT4_SIVCZ	Q5QFT4	chimpanzee	653	38	42.7	267	2	Q9K913_BACHD	Q9K913	bacillus ha
581	38	42.7	214	2	Q5QF04_SIVCZ	Q5QF04	chimpanzee	654	38	42.7	275	2	Q5YTJ1_NOCFA	Q5YTJ1	nocardia fa
582	38	42.7	214	2	Q5QFV6_SIVCZ	Q5QFV6	chimpanzee	655	38	42.7	278	2	Q84H03_PHOLU	Q84H03	photorhabdu
583	38	42.7	214	2	Q5QGB5_SIVCZ	Q5QGB5	chimpanzee	656	38	42.7	279	2	Q9GK11_SHEEP	Q9GK11	ovis aries
584	38	42.7	214	2	Q5TVK2_SIVCZ	Q5TVK2	chimpanzee	657	38	42.7	287	2	Q5OP14_ENTHI	Q5OP14	entamoeba h
585	38	42.7	214	2	Q5XLN0_9PLVG	Q5XLN0	simian-huma	658	38	42.7	292	2	Q9M2F6_ARATH	Q9M2F6	arabidopsis
586	38	42.7	214	2	Q6J3Q4_SIVCZ	Q6J3Q4	chimpanzee	659	38	42.7	293	2	Q8LC98_ARATH	Q8LC98	arabidopsis
587	38	42.7	214	2	Q76UX9_SIVCZ	Q76UX9	chimpanzee	660	38	42.7	298	2	Q60XY2_CAEBR	Q60XY2	caenorhabdi
588	38	42.7	214	2	Q76W8X_SIVCZ	Q76W8X	chimpanzee	661	38	42.7	298	2	Q5OM18_ENTHI	Q5OM18	entamoeba h
589	38	42.7	214	2	Q774X0_SIVCZ	Q774X0	simian immu	662	38	42.7	301	2	Q22804_CAEEL	Q22804	caenorhabdi
590	38	42.7	214	2	Q774X4_SIVCZ	Q774X4	simian immu	663	38	42.7	302	2	Q84WV7_ARATH	Q84WV7	arabidopsis
591	38	42.7	214	2	Q77Y25_9PLVG	Q77Y25	simian-huma	664	38	42.7	311	2	Q5E1C1_VIBF1	Q5E1C1	vibrio fisc
592	38	42.7	214	2	Q87707_SIVCZ	Q87707	chimpanzee	665	38	42.7	319	2	Q5ONK2_ENTHI	Q5ONK2	entamoeba h
593	38	42.7	214	2	Q88022_SIVCZ	Q88022	chimpanzee	666	38	42.7	323	1	AKIC3_HUMAN	P42330	h aldo-keto
594	38	42.7	214	2	Q88044_SIVCZ	Q88044	chimpanzee	667	38	42.7	323	1	PGFS1_BOVIN	P05980	bos taurus
595	38	42.7	214	2	Q88046_SIVCZ	Q88046	chimpanzee	668	38	42.7	323	1	PGFS2_BOVIN	P52897	bos taurus
596	38	42.7	214	2	Q88054_SIVCZ	Q88054	chimpanzee	669	38	42.7	328	2	Q5OM15_ENTHI	Q5OM15	entamoeba h
597	38	42.7	214	2	Q88056_SIVCZ	Q88056	chimpanzee	670	38	42.7	330	2	Q9SL59_ARATH	Q9SL59	arabidopsis
598	38	42.7	214	2	Q88061_SIVCZ	Q88061	chimpanzee	671	38	42.7	332	2	Q4JC41_SULAC	Q4JC41	sulfolobus
599	38	42.7	214	2	Q88063_SIVCZ	Q88063	chimpanzee	672	38	42.7	338	2	Q42SB2_NITEU	Q42SB2	nitrosomona
600	38	42.7	214	2	Q88067_SIVCZ	Q88067	chimpanzee	673	38	42.7	342	2	Q41J55_GIBZ	Q41J55	gibberella
601	38	42.7	214	2	Q88136_SIVCZ	Q88136	chimpanzee	674	38	42.7	352	2	Q17179_CAEEL	Q17179	caenorhabdi
602	38	42.7	214	2	Q88144_SIVCZ	Q88144	chimpanzee	675	38	42.7	358	2	Q6F7X7_ACIAD	Q6F7X7	acinetobact
603	38	42.7	214	2	Q89490_SIVCZ	Q89490	c simian i	676	38	42.7	359	2	Q98IK6_RHILO	Q98IK6	rhizobium l
604	38	42.7	214	2	Q89716_SIVCZ	Q89716	chimpanzee	677	38	42.7	361	2	Q8BKES_MOUSE	Q8BKES	mus musculu
605	38	42.7	214	2	Q89825_SIVCZ	Q89825	chimpanzee	678	38	42.7	372	2	Q75IQ5_ORYSA	Q75IQ5	oryza sativ
606	38	42.7	214	2	Q07391_SIVCZ	Q07391	chimpanzee	679	38	42.7	389	2	Q6ZPL2_MOUSE	Q6ZPL2	mus musculu
607	38	42.7	214	2	P89155_SIVCZ	P89155	chimpanzee	680	38	42.7	394	2	Q4WL37_ASFFU	Q4WL37	aspergillus
608	38	42.7	215	1	VIF_HV2BE	P18097	human immun	681	38	42.7	402	2	Q5CYR1_CRYPV	Q5CYR1	cryptospori
609	38	42.7	215	1	VIF_HV2CA	P24108	human immun	682	38	42.7	402	2	Q5CP17_CRYVO	Q5CP17	cryptospori
610	38	42.7	215	1	VIF_HV2D1	P17758	human immun	683	38	42.7	405	2	Q4INQ5_GBZ	Q4INQ5	gibberella
611	38	42.7	215	1	VIF_HV2G1	P18043	human immun	684	38	42.7	405	2	Q4TR85_TETNG	Q4TR85	tetracodon n
612	38	42.7	215	1	VIF_HV2K1	Q74121	human immun	685	38	42.7	407	2	Q8ALD2_BACTN	Q8ALD2	bacteroides
613	38	42.7	215	1	VIF_HV2N2	P05901	human immun	686	38	42.7	430	2	Q5FOI9_GLUJOX	Q5FOI9	gluconobact
614	38	42.7	215	1	VIF_HV2RO	P04595	human immun	687	38	42.7	430	2	Q5P0S3_AZOSE	Q5P0S3	azocarcus sp
615	38	42.7	215	1	VIF_HV2SB	P12452	human immun	688	38	42.7	431	2	Q4ZDF5_9VIRU	Q4ZDF5	bacterioph

689	38	42.7	437	2	Q9W325_DROME	Q9w325 drosophila	762	38	42.7	656	2	Q59G95_HUMAN	Q59g95 homo sapien
690	38	42.7	437	2	Q61EP2_CABER	Q61ep2 caenorhabdi	763	38	42.7	657	2	Q5LNB6_SILPO	Q5lnb6 silicbacte
691	38	42.7	438	1	ALG3_MOUSE	Q8k2a8 mus musculu	764	38	42.7	660	2	Q5F970_NEIMA	Q5f970 neisseria g
692	38	42.7	451	2	Q76410_CABEL	Q76410 caenorhabdi	765	38	42.7	660	2	Q9JU57_NEIMA	Q9ju57 neisseria m
693	38	42.7	454	2	Q17833_CABEL	Q17833 caenorhabdi	766	38	42.7	661	2	Q9M3F0_ARATH	Q9m3f0 arabidopsis
694	38	42.7	454	2	Q7ZVD6_XENLA	Q7zvd6 xenopus tro	767	38	42.7	664	2	Q9M3F0_ARATH	Q9m3f0 arabidopsis
695	38	42.7	454	2	Q5U229_XENR	Q5u229 xenopus tro	768	38	42.7	666	2	Q4N581_THEPA	Q4n581 theileria p
696	38	42.7	456	2	Q969V2_HUMAN	Q969v2 homo sapien	769	38	42.7	668	2	Q9CK43_PASMU	Q9ck43 haemophilus
697	38	42.7	456	2	Q8R5N4_PONPY	Q8r5n4 pongo pygma	770	38	42.7	669	2	Q4N581_THEPA	Q4n581 theileria p
698	38	42.7	456	2	Q80UR9_MOUSE	Q80ur9 mus musculu	771	38	42.7	669	2	Q4N581_THEPA	Q4n581 theileria p
699	38	42.7	458	2	Q5B4V9_EMENI	Q5b4v9 aspergillus	772	38	42.7	675	2	Q4QJN6_HAE18	Q4qjn6 haemophilus
700	38	42.7	459	2	Q5ZK35_CHICK	Q5zk35 gallus gall	773	38	42.7	686	2	Q9J261_NEIME	Q9j261 neisseria m
701	38	42.7	463	2	Q4IQ88_GIBBE	Q4iq88 gibberella	774	38	42.7	691	2	Q5FC25_CABEL	Q5fc25 caenorhabdi
702	38	42.7	463	2	Q4IQ88_GIBBE	Q4iq88 gibberella	775	38	42.7	709	2	Q4PD10_USTMA	Q4pd10 ustilago ma
703	38	42.7	467	2	Q4MLX8_BACCE	Q4mlx8 bacillus ce	776	38	42.7	722	2	Q6L3U7_SOLDE	Q6l3u7 solanum dem
704	38	42.7	467	2	Q4RLX8_TETNG	Q4rlx8 tetraodon n	777	38	42.7	743	2	Q5H8Y9_HUMAN	Q5h8y9 homo sapien
705	38	42.7	468	1	Y1107_HAEIN	Q57007 haemophilus	778	38	42.7	747	2	Q602C8_MYCHY	Q602c8 mycoplasma
706	38	42.7	468	2	Q9HCE5_HUMAN	Q9hce5 homo sapien	779	38	42.7	759	1	YEHM_ECOLI	Yehm escherichia
707	38	42.7	468	2	Q4QLI4_HAE18	Q4qli4 haemophilus	780	38	42.7	759	1	Q7UCAL_SHIFL	Q7ucal shigella fl
708	38	42.7	470	2	Q419V6_GIBZE	Q419v6 gibberella	781	38	42.7	759	1	Q83KG7_SHIFL	Q83kg7 shigella fl
709	38	42.7	471	1	CYP8_SCHPO	Q721X1_THER2	782	38	42.7	771	2	Q4SWM4_TETNG	Q4swm4 tetraodon n
710	38	42.7	474	2	Q4RLG9_TETNG	Q4rlg9 schizosacch	783	38	42.7	772	2	Q4SWM4_TETNG	Q4swm4 tetraodon n
711	38	42.7	480	2	Q7TVG7_MYCBO	Q7tvgr7 mycobacteri	784	38	42.7	772	2	Q5H8Y9_HUMAN	Q5h8y9 homo sapien
712	38	42.7	480	2	Q69734_MYCTU	Q69734 mycobacteri	785	38	42.7	793	2	Q6S404_ECOLI	Q6s404 escherichia
713	38	42.7	480	2	Q8BR69_MOUSE	Q8br69 mus musculu	786	38	42.7	805	1	L100_ADE02	L100 adeo
714	38	42.7	481	2	Q7VDD7_PROMA	Q7vdk7 prochlorococ	787	38	42.7	807	1	L100_ADE05	L100 adeo
715	38	42.7	484	2	Q7U4U8_SYNPX	Q7u4u8 synechococ	788	38	42.7	807	2	Q5VGF3_9ADEN	Q5vgf3 9aden
716	38	42.7	486	2	Q6C4F5_YARLI	Q6c4f5 yarrowia li	789	38	42.7	807	2	Q71BW5_ADE01	Q71bw5 human adeno
717	38	42.7	486	2	Q8L4E4_ORYSA	Q8l4e4 oryza sativ	790	38	42.7	845	2	Q6H965_ONCMY	Q6h965 oncorhynch
718	38	42.7	486	2	Q8GBS9_SYNPX	Q8gbs9 synechococ	791	38	42.7	851	2	Q14031_SCHPO	Q14031 schizosacch
719	38	42.7	489	2	Q6CRN1_KLUJA	Q6crn1 kluyveromyc	792	38	42.7	865	2	Q61EQ5_CABER	Q61eq5 caenorhabdi
720	38	42.7	493	2	Q6CRN1_KLUJA	Q6crn1 kluyveromyc	793	38	42.7	881	2	Q3LPG3_ARATH	Q3lpg3 arabidopsis
721	38	42.7	495	2	Q8GB94_PROMA	Q8gb94 prochlorococ	794	38	42.7	892	1	HULA_YEAST	Hula yeast
722	38	42.7	495	2	Q7V5C0_PROMM	Q7v5c0 prochlorococ	795	38	42.7	906	2	Q8NF52_HUMAN	Q8nf52 homo sapien
723	38	42.7	498	2	Q7S109_NEUCR	Q7s109 neurospora	796	38	42.7	915	1	Q8NFS3_HUMAN	Q8nfs3 homo sapien
724	38	42.7	501	2	Q93AK1_VIRPA	Q93ak1 virgibacill	797	38	42.7	915	1	MGR7_MOUSE	Mgr7 mouse
725	38	42.7	503	2	Q6PDRO_MOUSE	Q6pdro mus musculu	798	38	42.7	915	1	MGR7_MOUSE	Mgr7 mouse
726	38	42.7	503	2	Q8BG07_MOUSE	Q8bg07 m mus muscu	799	38	42.7	915	1	MGR7_MOUSE	Mgr7 mouse
727	38	42.7	504	2	Q6FP76_CANGA	Q6fp76 candida gla	800	38	42.7	922	2	Q5RD08_PONPY	Q5rd08 pongo pygma
728	38	42.7	509	2	Q60WV9_CABER	Q60wv9 caenorhabdi	801	38	42.7	924	2	Q8NF84_HUMAN	Q8nf84 homo sapien
729	38	42.7	510	1	YM67_CABEL	Q34528 caenorhabdi	802	38	42.7	952	2	Q7EZL3_ORYSA	Q7ezl3 oryza sativ
730	38	42.7	511	2	Q53ND8_ORYSA	Q53nd8 oryza sativ	803	38	42.7	1017	1	LRG1_YEAST	Lrg1 yeast
731	38	42.7	515	2	Q8CB11_MOUSE	Q8cb11 mus musculu	804	38	42.7	1038	2	Q9VWP9_DROME	Q9vwp9 drosophila
732	38	42.7	515	2	Q8CB11_MOUSE	Q8cb11 mus musculu	805	38	42.7	1039	2	Q52G03_MAGGR	Q52g03 magnaporth
733	38	42.7	517	2	Q51UA9_MAGGR	Q51ua9 magnaporth	806	38	42.7	1052	1	FGFR2_DROME	FGFR2 drosophila
734	38	42.7	519	2	Q8RYE3_ARATH	Q8rye3 arabidopsis	807	38	42.7	1062	2	Q8NQX3_DROME	Q8nqx3 drosophila
735	38	42.7	525	2	Q6OR72_CABER	Q6or72 caenorhabdi	808	38	42.7	1063	2	Q7LJES_HUMAN	Q7lj3es homo sapien
736	38	42.7	525	2	Q17832_CABEL	Q17832 caenorhabdi	809	38	42.7	1066	2	Q9NZS3_HUMAN	Q9nzs3 homo sapien
737	38	42.7	527	2	Q418L4_TETNG	Q418l4 tetraodon n	810	38	42.7	1157	2	Q7QI35_ANOGA	Q7qi35 anopheles g
738	38	42.7	529	2	Q41N09_GIBZE	Q41n09 gibberella	811	38	42.7	1177	2	Q5AX46_EMENI	Q5ax46 aspergillus
739	38	42.7	531	2	Q8G5A2_BIFLO	Q8g5a2 bifidobacte	812	38	42.7	1180	2	Q7S1J3_ORYSA	Q7s1j3 oryza sativ
740	38	42.7	532	2	Q18247_CABEL	Q18247 caenorhabdi	813	38	42.7	1209	2	Q59GT4_HUMAN	Q59gt4 homo sapien
741	38	42.7	532	2	Q5FC26_CABEL	Q5fc26 caenorhabdi	814	38	42.7	1209	2	Q9NSW6_HUMAN	Q9nsw6 homo sapien
742	38	42.7	539	1	TYRO_ASFOR	Q00234 aspergillus	815	38	42.7	1215	1	HDAC6_HUMAN	HDAC6 human
743	38	42.7	539	2	Q8YLJ0_ANASP	Q8ylj0 anabaena sp	816	38	42.7	1215	1	HDAC6_HUMAN	HDAC6 human
744	38	42.7	562	2	Q60PS4_CABER	Q60ps4 caenorhabdi	817	38	42.7	1226	2	Q6H0K6_9HIV2	Q6h0k6 human immu
745	38	42.7	565	2	Q9M195_ARATH	Q9m195 arabidopsis	818	38	42.7	1228	2	Q9PH02_USTMA	Q9ph02 ustilago ma
746	38	42.7	566	2	Q5U372_BRARE	Q5u372 brachydanio	819	38	42.7	1233	2	Q94975_HUMAN	Q94975 homo sapien
747	38	42.7	569	2	Q7Q2R2_ANOGA	Q7q2r2 anopheles g	820	38	42.7	1313	2	Q9ZRG2_SOLTU	Q9zrg2 solanum tub
748	38	42.7	576	2	Q73S93_MYCPA	Q73s93 mycobacteri	821	38	42.7	1344	2	Q7EZL2_ORYSA	Q7ezl2 oryza sativ
749	38	42.7	580	2	Q4PLQ5_USTMA	Q4plq5 ustilago ma	822	38	42.7	1349	2	Q8GU78_ORYSA	Q8gu78 oryza may
750	38	42.7	581	2	Q50Z30_ENTHI	Q50z30 entamoeba h	823	38	42.7	1394	2	Q6UNK5_MAIZE	Q6unk5 zea mays
751	38	42.7	587	2	Q5FC23_CABEL	Q5fc23 caenorhabdi	824	38	42.7	1402	2	Q6UC91_SORBI	Q6uc91 sorghum bic
752	38	42.7	588	2	Q529B9_MAGGR	Q529b9 magnaporth	825	38	42.7	1419	2	Q4RNP2_TETNG	Q4rnp2 tetraodon n
753	38	42.7	599	2	Q7PXS8_ANOGA	Q7pxs8 anopheles g	826	38	42.7	1423	2	Q4HUF6_GIBZE	Q4huf6 gibberella
754	38	42.7	606	1	NUSM_BRARE	Q9mlv0 brachydanio	827	38	42.7	1608	2	Q527E4_MAGGR	Q527e4 magnaporth
755	38	42.7	611	2	Q9BL51_CABEL	Q9bl51 caenorhabdi	828	38	42.7	1620	1	ABL_DROME	ABL drosophila
756	38	42.7	619	2	Q7T302_BRARE	Q7t302 brachydanio	829	38	42.7	1939	2	Q4QIJ2_LEIMA	Q4qij2 leishmania
757	38	42.7	622	2	Q9HEL3_NEUCR	Q9hel3 neurospora	830	38	42.7	2200	2	Q7XP97_ORYSA	Q7xp97 oryza sativ
758	38	42.7	624	2	Q5FC24_CABEL	Q5fc24 caenorhabdi	831	38	42.7	4061	2	Q60M30_CABER	Q60m30 caenorhabdi
759	38	42.7	630	2	Q7S3D2_NEUCR	Q7s3d2 neurospora	832	38	42.7	4523	2	Q61F02_CABER	Q61f02 caenorhabdi
760	38	42.7	632	2	Q6ZSV8_HUMAN	Q6zsv8 homo sapien	833	37.5	42.1	99	2	Q4VX86_HUMAN	Q4vx86 homo sapien
761	38	42.7	644	2	Q7S7W3_NEUCR	Q7s7w3 neurospora	834	37.5	42.1	117	1	CT166_HUMAN	CT166 homo sapien

835	37.5	42.1	229	2	P94406_BACSU	P94406 bacillus su	908	37	41.6	164	2	Q6SZN6_RHOFA	Q6szn6 rhodococcus
836	37.5	42.1	251	2	O18207_GABEL	O18207 caenorhabdi	909	37	41.6	169	2	Q7UJ04_RHOBA	Q7uj04 rhodopirell
837	37.5	42.1	351	2	Q4IAQ5_GIBZEL	Q4iaq5 gibberella	910	37	41.6	172	2	Q64BU6_PARCH	Q64bu6 uncultured
838	37.5	42.1	351	2	Q4SVA5_TETNG	Q4svas tetraodon n	911	37	41.6	172	2	Q87Y73_PSESM	Q87y73 pseudomonas
839	37.5	42.1	379	1	Y4XO_RHISN	P55707 rhizobium s	912	37	41.6	174	2	Q4TGC7_TETNG	Q4tgc7 tetraodon n
840	37.5	42.1	395	2	Q746D8_THET2	Q746d8 thermus the	913	37	41.6	179	2	Q5CSX7_CRYPV	Q5csx7 cryptospori
841	37.5	42.1	395	2	Q53W07_THET8	Q53w07 thermus the	914	37	41.6	179	2	Q5CKH4_CRYHO	Q5ckh4 cryptospori
842	37.5	42.1	406	2	Q8ROB9_RHIFR	Q8rb9 rhizobium f	915	37	41.6	184	2	Q6IIG7_DROME	Q6iig7 drosophila
843	37.5	42.1	531	2	Q5SNV6_HUMAN	Q5snv6 homo sapien	916	37	41.6	188	2	Q7MAN1_HUMAN	Q7man1 homo sapien
844	37.5	42.1	533	2	Q5SQX0_CRYNE	Q5sqx0 cryptococcus	917	37	41.6	197	2	Q52AR2_MAGGR	Q52ar2 magnaprote
845	37.5	42.1	533	2	Q5KF88_CRYNE	Q5kf88 cryptococcus	918	37	41.6	198	2	Q899L4_CLOTE	Q899l4 clostridium
846	37.5	42.1	569	2	Q55F76_DICDI	Q55f76 dictyosteli	919	37	41.6	198	2	Q6AAM8_PROAC	Q6aam8 propionibac
847	37.5	42.1	577	2	Q74ZX1_ASHGO	Q74zx1 ashbya goss	920	37	41.6	201	2	Q86VK6_HUMAN	Q86vk6 homo sapien
848	37.5	42.1	580	2	Q55IH6_CRYNE	Q55ih6 cryptococcus	921	37	41.6	208	2	Q5QGR1_MASBA	Q5qgr1 nastiganceb
849	37.5	42.1	580	2	Q5KJH3_CRYNE	Q5kjas cryptococcus	922	37	41.6	213	2	Q81431_ARATH	Q81431 arabidopsis
850	37.5	42.1	596	2	Q6LP02_PHOPR	Q6lp02 photobacter	923	37	41.6	213	2	Q6GZY7_FREDI	Q6gzy7 fremyella d
851	37.5	42.1	599	2	Q6AIP6_VIBCH	Q6aip6 vibrio chol	924	37	41.6	223	2	Q9H368_HUMAN	Q9h368 homo sapien
852	37.5	42.1	615	2	Q8NDA9_HUMAN	Q8nda9 homo sapien	925	37	41.6	223	2	Q54U35_DICDI	Q54u35 dictyosteli
853	37.5	42.1	615	2	Q5NDV7_HUMAN	Q5ndv7 homo sapien	926	37	41.6	230	2	Q984B0_RHIL0	Q984b0 rhizobium l
854	37.5	42.1	652	2	Q9L0P7_STRCO	Q9lop7 streptomyce	927	37	41.6	231	2	Q8M834_9TURB	Q8m834 microstomum
855	37.5	42.1	716	2	Q5R2A7_VIRU	Q5r2a7 canine minu	928	37	41.6	235	2	Q7TFV9_RHECM6	Q7tfv9 rhesus cyto
856	37.5	42.1	716	2	Q8QQV7_VIRU	Q8qqv7 canine minu	929	37	41.6	236	2	Q5L204_GEOKA	Q5l204 geobacillus
857	37.5	42.1	745	2	Q8NDA9_HUMAN	Q8nda9 homo sapien	930	37	41.6	238	2	Q5HYD4_HUMAN	Q5hyd4 homo sapien
858	37.5	42.1	752	2	Q7XOW6_ORYSA	Q7xow6 oryza sativ	931	37	41.6	239	2	Q6ZNV3_HUMAN	Q6znv3 homo sapien
859	37.5	42.1	759	2	Q4SPZ5_TETNG	Q4sfz5 tetraodon n	932	37	41.6	241	2	Q4MW43_BACCE	Q4mw43 bacillus ce
860	37.5	42.1	827	2	Q5SNV9_HUMAN	Q5snv9 homo sapien	933	37	41.6	243	2	Q5VY54_HUMAN	Q5vy54 homo sapien
861	37.5	42.1	853	2	Q6FX46_CANGA	Q6fx46 candida gla	934	37	41.6	243	2	Q9SK17_ARATH	Q9sk17 arabidopsis
862	37.5	42.1	895	2	Q5KF70_CRYNE	Q5kf70 cryptococcus	935	37	41.6	243	2	Q4IWO0_AZOVI	Q4iwo0 azotobacter
863	37.5	42.1	920	2	Q5KC96_CRYNE	Q5kc96 cryptococcus	936	37	41.6	244	1	YMF16_MARPO	Ymf16 marchantia
864	37.5	42.1	932	2	Q5KBU9_CRYNE	Q5kbu9 cryptococcus	937	37	41.6	247	2	Q9DCZ2_MOUSE	Q9dcz2 mus musculu
865	37.5	42.1	932	2	Q55ZF3_CRYNE	Q55zf3 cryptococcus	938	37	41.6	247	2	Q5SR14_HUMAN	Q5sr14 homo sapien
866	37.5	42.1	934	1	CO6_HUMAN	P13671 crypto	939	37	41.6	249	2	Q8G439_BIFLO	Q8g439 bifidobacte
867	37.5	42.1	934	1	CO6_PANTR	P61134 pan troglod	940	37	41.6	249	2	Q8BY63_MOUSE	Q8by63 mus musculu
868	37.5	42.1	934	1	CO6_PONPY	P61135 pongo pygma	941	37	41.6	251	2	Q8NAJ3_HUMAN	Q8naj3 homo sapien
869	37.5	42.1	935	2	Q6IR82_XENLA	Q6ir82 xenopus lae	942	37	41.6	252	2	Q7M4N2_HUMAN	Q7m4n2 homo sapien
870	37.5	42.1	999	2	Q7SIV2_NEUCR	Q7siv2 neosporea	943	37	41.6	252	2	Q5LM33_SILPO	Q5lm33 silicibacte
871	37.5	42.1	1680	2	Q5RFP8_PONPY	Q5rfs8 pongo pygma	944	37	41.6	256	2	Q99PA2_RAT	Q99pa2 rattus norv
872	37.5	42.1	2954	2	Q4IRV3_GIBZE	Q4irv3 gibberella	945	37	41.6	258	2	Q9SHS4_ARATH	Q9shs4 arabidopsis
873	37	41.6	41	2	Q5C125_SCHJA	Q5c125 schistosoma	946	37	41.6	263	2	Q4LI21_9BURK	Q4li21 burkholderi
874	37	41.6	45	2	Q5C4T1_SCHJA	Q5c4t1 schistosoma	947	37	41.6	268	2	Q8LF12_ARATH	Q8lf12 arabidopsis
875	37	41.6	58	2	Q7S7V8_NEUCR	Q7s7v8 neosporea	948	37	41.6	271	2	Q9FJN3_ARATH	Q9fjn3 arabidopsis
876	37	41.6	64	1	SIX3_MESMA	O17231 mesobuthus	949	37	41.6	272	2	Q4YXS4_PLABE	Q4yxs4 plasmodium
877	37	41.6	64	1	SIX3_MESMA	O17231 mesobuthus	950	37	41.6	273	2	Q5NVN2_AZOSE	Q5nvn2 azoarcus sp
878	37	41.6	66	2	Q4THS5_TETNG	Q4tdhs tetraodon n	951	37	41.6	274	2	Q8IJC2_PLAF7	Q8ijc2 plasmodium
879	37	41.6	69	2	Q6RCW5_HOVIN	Q6rcw5 bos taurus	952	37	41.6	277	2	Q639K2_BACCD	Q639k2 bacillus ce
880	37	41.6	75	2	Q8JTA7_9VIRU	Q8jta7 mirabilis m	953	37	41.6	277	2	Q6NIZ9_CORDI	Q6niz9 corynebacte
881	37	41.6	76	2	Q9T115_9CAUD	Q9t115 bacterioph	954	37	41.6	278	2	Q6ZUW1_HUMAN	Q6zuw1 homo sapien
882	37	41.6	85	1	ABP1_MESMA	P15228 mesobuthus	955	37	41.6	286	2	Q59GU2_HUMAN	Q59gu2 homo sapien
883	37	41.6	85	1	SIX2_BUTJU	P24336 buthotus ju	956	37	41.6	288	2	Q5OQP2_ENTHI	Q5oqp2 entamoeba h
884	37	41.6	85	2	Q8PSP2_METWA	Q8psp2 methanosarc	957	37	41.6	295	1	CHO_ECOLI	Q8xdz7 escherichia
885	37	41.6	86	1	LCR7V6_ARATH	P82785 arabidopsis	958	37	41.6	295	1	CHO_SHIFL	P76213 escherichia
886	37	41.6	91	2	Q4RH10_TETNG	Q4rh10 tetraodon n	959	37	41.6	299	2	Q4NV03_9DELTA	P59361 shigella fl
887	37	41.6	93	1	LST1_MACMU	Q5tm23 macaca mula	960	37	41.6	299	2	Q4NV03_9DELTA	Q4nv03 anaeromyxob
888	37	41.6	98	2	Q9W4K3_DROSOPH	Q9w4k3 drosophila	961	37	41.6	305	2	Q6ZOA8_ORYSA	Q6zoa8 oryza sativ
889	37	41.6	102	2	Q9GMW1_MACFA	Q9gmw1 macaca fasc	962	37	41.6	307	2	Q6FNN9_CANGA	Q6fnn9 candida gla
890	37	41.6	109	2	Q6CTQ7_KLUJA	Q6ctq7 kluyveromyc	963	37	41.6	308	2	Q8INY0_ANASP	Q8iny0 anaebana sp
891	37	41.6	111	2	Q6Z6R9_ORYSA	Q6z6r9 oryza sativ	964	37	41.6	309	1	T2R49_PONPY	Q645v6 pongo pygma
892	37	41.6	113	2	Q6PS66_9CARY	Q6ps66 haloxylon a	965	37	41.6	311	2	Q5CFU5_CRYHO	Q5cfu5 cryptospori
893	37	41.6	113	2	Q5ZKH2_CHICK	Q5zkh2 gallus gall	966	37	41.6	311	2	Q5CXU5_CRYPV	Q5cxu5 cryptospori
894	37	41.6	119	2	Q8BSU9_MOUSE	Q8bsu9 mus musculu	967	37	41.6	313	2	Q7P248_ANOGA	Q7p248 anopheles g
895	37	41.6	130	2	Q7Z2T1_HUMAN	Q7z2t1 homo sapien	968	37	41.6	313	2	Q8VY22_LEPIN	Q8vy22 leptospira
896	37	41.6	138	2	Q853E3_9CAUD	Q853e3 mycobacteri	969	37	41.6	313	2	Q7ZQH9_LEPIC	Q7zqh9 leptospira
897	37	41.6	138	2	Q8CCF6_MOUSE	Q8ccf6 mus musculu	970	37	41.6	313	2	Q9S4G4_LEPIN	Q9s4g4 leptospira
898	37	41.6	138	2	Q5YFA7_9VIRU	Q5yfa7 singapore g	971	37	41.6	315	2	Q4TSD7_9SPHN	Q4tld7 erythrobact
899	37	41.6	144	2	Q6IIV8_DROME	Q6iiv8 drosophila	972	37	41.6	318	2	Q6LQL6_PHOPR	Q6lql6 photobacter
900	37	41.6	148	2	Q6AAL5_PROAC	Q6aal5 propionibac	973	37	41.6	318	2	Q8VYJ8_ANASP	Q8vyj8 anaebana sp
901	37	41.6	151	2	Q9G6Z2_9TURB	Q9g6z2 microstomum	974	37	41.6	318	2	Q6AYQ2_RAT	Q6ayq2 rattus norv
902	37	41.6	154	2	Q8USF5_AGRYS	Q8usf5 agrobacteri	975	37	41.6	319	2	Q8GGP1_STRAZ	Q8gppi streptomyce
903	37	41.6	159	2	Q6Z6S0_ORYSA	Q6z6s0 oryza sativ	976	37	41.6	323	1	AKIC1_HUMAN	Q04828 h aldo-keto
904	37	41.6	160	2	Q63P47_BURPS	Q63p47 burkholderi	977	37	41.6	323	1	AKIC1_MACFA	Q951h7 macaca fasc
905	37	41.6	161	2	Q63NX7_BURPS	Q63nx7 burkholderi	978	37	41.6	323	1	AKIC1_MACPU	Q951h6 macaca fusc
906	37	41.6	161	2	Q4V2A5_BURMA	Q4v2a5 burkholderi	979	37	41.6	323	1	AKIC1_PONPY	Q5rsq0 pongo pygma
907	37	41.6	163	2	Q6Z7Z0_ELOSA	Q6z7z0 elops sauru	980	37	41.6	323	1	AKIC2_HUMAN	P52895 h aldo-keto


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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21887392; PubMed=11890535; DOI=10.1007/s705-002-8332-5;
RA Han S.S., Yoshida Y., Karasev A.V., Iwanami T.;
RT "Nucleotide sequence of a Japanese isolate of Squash mosaic virus.";
RL Arch. Virol. 147:437-443(2002).
DR EMBL; AB054688; BAB62139.1; -; Genomic_RNA.
DR MEROPS; C03.003; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0031079; F:picornain 3C activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR000199; Pept_C3_picorn.
DR InterPro; IPR004004; Pept_Calici.
DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR Pfam; PF00548; Peptidase_C3; 1.
DR Pfam; PF00680; RdRP_1; 1.
DR Pfam; PF00910; RNA helicase; 1.
DR PRINTS; PR00918; CALICVIRUSNS.
DR ProDom; PD001125; Pept_C3_picorn; 1.
KW Polyprotein.
SQ SEQUENCE 1858 AA; 209972 MW; B344D1FC83641829 CRC64;

Query Match 58.4%; Score 52; DB 2; Length 1858;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCTWTE 9
DB 1033 WDVECDWE 1041

RESULT 4
Q6CAB0 YARLI PRELIMINARY; PRT; 260 AA.
AC Q6CAB0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similar to tr|Q05533 Saccharomyces cerevisiae YDR287w (Fragment).
GN OrderedLocNames=YALI0D04378g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin L., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Keraest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller R.,
RA Nicaud J.-M., Nikolski M., Orlas S., Ozier-Kalogeropoulos O.,
RA Pellenn S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
DR EMBL; CR382130; CAG80590.1; -; Genomic DNA.
DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatase. .; IEA.
DR InterPro; IPR000760; Inositol_P.

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DR Pfam; PF00459; Inositol_P; 1.
DR PRINTS; PR00378; INOSPHPTASE.
DR ProDom; PD023420; Inositol_P; 1.
DR PROSITE; PS00629; IMP_1; 1.
DR PROSITE; PS00630; IMP_2; 1.
KW Complete proteome.
FT NON_TER 1
SQ SEQUENCE 260 AA; 27973 MW; 8891E53F0AD39337 CRC64;

Query Match 57.3%; Score 51; DB 2; Length 260;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWTEC 11
DB 190 WEGGCWADV 200

RESULT 5
Q4WEX3 ASPFU PRELIMINARY; PRT; 292 AA.
AC Q4WEX3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Outg protein.
GN ORFNames=Afu3g04250;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohammad Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penalta M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Varquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAHF01000010; EAL86704.1; -; Genomic DNA.
SQ SEQUENCE 292 AA; 31770 MW; B1EA643830F87A0A CRC64;

Query Match 57.3%; Score 51; DB 2; Length 292;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWTEC 11
DB 223 WEGGCWADV 233

RESULT 6
Q05533_YEAST

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RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACW01000107; EAA67731.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 297 AA; 31987 MW; 911CC4DD44584027 CRC64;
Query Match 57.3%; Score 51; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETC 11
Db 227 WEGGCWAWDVC 237
RESULT 9
Q4SKD7_TETNG PRELIMINARY; PRT; 269 AA.
ID Q4SKD7;
AC Q4SKD7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 13 SCAR14566, whole genome shotgun sequence.
OS ORFNames=GSTENG0016780001;
GN Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Besak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014566; CAF98895.1; -; Genomic DNA.
SQ SEQUENCE 269 AA; 30469 MW; 2063045FB3AFC69 CRC64;
Query Match 56.2%; Score 50; DB 2; Length 269;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CWTWETC 11
Db 218 CWTWETC 224
RESULT 10
Q5BLJ1_EMENI PRELIMINARY; PRT; 567 AA.
ID Q5BLJ1;
AC Q5BLJ1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN5589.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel V., Collymore A., Cook A., Cooke P., Corum B., DeAtellano K.,
RA Diaz J.S., Dodge S., Pooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Minova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome sequence of Aspergillus nidulans."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the FGK kinase family.
DR EMBL; AACD01000096; EAA62232.1; -; Genomic DNA.
DR GO; GO:0004370; F:glycerol kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0006072; P:glycerol-3-phosphate metabolism; IEA.
KW Hypothetical protein; Kinase; transferase.
SQ SEQUENCE 567 AA; 62914 MW; 88EBC97DC798DEAD CRC64;
Query Match 56.2%; Score 50; DB 2; Length 567;
Best Local Similarity 80.0%; Pred. No. 56;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 VLCWTWETC 12
Db 138 VLCWDWETGE 147
RESULT 11
Q9C693_ARATH PRELIMINARY; PRT; 395 AA.
ID Q9C693;
AC Q9C693;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T8L23.7.
GN Name=T8L23.7;

```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
RA Wu D., Maiz R., Rowan C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC097933; AAG50749.1; -; Genomic_DNA.
DR PIR; B96610; B96610.
DR InterPro; IPR004299; MBOAT fam.
DR InterPro; IPR001202; WW Rep5_WWP.
DR Pfam; PF03062; MBOAT; 1;
DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 395 AA; 46301 MW; B798F34663E3E62D3 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 395;
Best Local Similarity 54.5%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCTWETC 11
Db 284 WKLLSWALTC 294

RESULT 12
QRY80 ARATH PRELIMINARY; PRT; 533 AA.
AC QRY80;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein Atlg57600.
GN Name=Atlg57600;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldmich A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074538; AAL69506.1; -; mRNA.
DR InterPro; IPR004299; MBOAT fam.
DR Pfam; PF03062; MBOAT; 1;
DR PROSITE; PS01159; WW_DOMAIN_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 533 AA; 62791 MW; 5C497EF542EB9A66 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 533;
Best Local Similarity 54.5%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCTWETC 11
Db 422 WKLLSWALTC 432

RESULT 13
Q8CBK5_MOUSE PRELIMINARY; PRT; 460 AA.
ID Q8CBK5_MOUSE PRELIMINARY;

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AC Q8CBK5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length
DE enriched library, clone:B830029I03 product:hypothetical G-protein beta
DE WD-40 repeats containing protein, full insert sequence.
GN Name=Wdr41;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC MEDLINE=20459374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format

```


RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

[6]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK046853; BAC32897.1; -; mRNA.
DR Ensembl; ENSMUSG0000042015; Mus musculus.
DR MGI; MGI:2445123; Wdr41.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS00678; WD_REPEATS_2; 3.
DR PROSITE; PS00678; WD_REPEATS_3; 3.
DR PROSITE; PS00678; WD_REPEATS_REGION; 2.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 460 AA; 51538 MW; 7387EB4F6EBD9AF3 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 460;

Best Local Similarity 53.8%; Pred. No. 89;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLCTWETFCR 13

DB 248 WDALDWTVOACER 260

RESULT 14

Q8CAZO MOUSE

ID Q8CAZO MOUSE PRELIMINARY; PRT; 138 AA.

AC Q8CAZO;

DT 01-WAR-2003 (T-EMBLrel. 23, Created)

DT 01-WAR-2003 (T-EMBLrel. 23, Last sequence update)

DT 01-WAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched

DE library, clone: A030008J09 product: hypothetical protein, full insert

DE sequence.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK037195; BAC29746.1; -; mRNA.
DR Ensembl; ENSMUSG0000054258; Mus musculus.
KW Hypothetical protein.
SQ SEQUENCE 138 AA; 15270 MW; 175C0698CF8BA926 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 138;

Best Local Similarity 75.0%; Pred. No. 39;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LCMTWETC 11

DB 38 LCMTWVC 45

RESULT 15

P79899 ONCMY
ID P79899 ONCMY PRELIMINARY; PRT; 236 AA.
AC P79899;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Pentraxin precursor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hepatic;
RX MEDLINE=97131713; PubMed=8977214;
RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
RA Whitehead A.S.;
RT "Acute phase proteins in Salmonids. Evolutionary analyses and acute
phase response.";
RT J. Immunol. 158:384-392(1997).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; X93185; CAA67764.1; -; mRNA.
DR HSSP; P02743; 1SAC.
DR InterPro; IPR001759; Pentaxin.
DR PANTHER; PTHR19277; Pentaxin; 1.
DR Pfam; PF00354; Pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.
DR ProDom; PD002153; Pentaxin; 1.
DR ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 236 pentraxin.
SQ SEQUENCE 236 AA; 26836 MW; 7F39A5F559025857 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 236;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTWT 10
| :|||:::
DB 116 WISICWTWDS 125

RESULT 16
P79905 SALSA
ID P79905 SALSA PRELIMINARY; PRT; 236 AA.
AC P79905;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Pentraxin precursor.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hepatic;
RX MEDLINE=97131713; PubMed=8977214;
RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.,
RA Whitehead A.S.;
RT "Acute phase proteins in Salmonids. Evolutionary analyses and acute
phase response.";
RT J. Immunol. 158:384-392(1997).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; X93386; CAA67765.1; -; mRNA.
DR HSSP; P02741; 1LJ7.
DR InterPro; IPR001759; Pentaxin.
DR PANTHER; PTHR19277; Pentaxin; 1.
DR Pfam; PF00354; Pentaxin; 1.
DR PRINTS; PR00895; PENTAXIN.

ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00159; PTX; 1.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 236 Pentraxin.
SQ SEQUENCE 236 AA; 26787 MW; FA69D8A65ASB9BE7 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 236;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTWT 10
| :|||:::
DB 116 WISICWTWDS 125

RESULT 17
Q7S2U5 NEUCR PRELIMINARY; PRT; 1026 AA.
ID Q7S2U5 NEUCR PRELIMINARY;
AC Q7S2U5;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU09030.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Maucelli E., Bielke C., Rudd S., Frisman D.,
RA Kryzstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDbj whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AABX01000418; EAA29741.1; -; Genomic DNA.
DR EMBL; AABX01000418; EAA29741.1; -; Genomic DNA.
SQ SEQUENCE 1026 AA; 115083 MW; 47E9028AE5321A7F CRC64;

Query Match 52.8%; Score 47; DB 2; Length 1026;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
| :|||:
DB 358 WSVICWEW 365

RESULT 18
Q4S5E2 TETNG PRELIMINARY; PRT; 137 AA.
ID Q4S5E2 TETNG PRELIMINARY;
AC Q4S5E2;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chromosome 19 SCAP14731, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00023773001;

OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Actinomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 RN NCBI_TaxID=99883;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet P., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014731; JG04140.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 137 AA; 15257 MW; 73E59F2F6A647F7D CRC64;
 Query Match 51.7%; Score 46; DB 2; Length 137;
 Best Local Similarity 62.5%; Pred. No. 54;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 CWTWETCE 12
 DB 108 CWMNTQ 115
 RESULT 19
 OS Q9QLJ0_NPVMC
 ID Q9QLJ0_NPVMC PRELIMINARY; PRT; 173 AA.
 AC Q9QLJ0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mamestra configurata nucleopolyhedrovirus (MaconPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=191492;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=90/2;
 RX MEDLINE=37163493; PubMed=9010313;
 RA Li S., Erlandson M., Moody D., Gillett C.;
 RT "A physical map of the Mamestra configurata nucleopolyhedrovirus
 RT genome and sequence analysis of the polyhedrin gene.";
 RL J. Gen. Virol. 78:265-271(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=90/2;
 RX MEDLINE=21884635; PubMed=11886270; DOI=10.1006/viro.2001.1313;
 RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlandson M.;
 RT "Sequence and organization of the Mamestra configurata
 RT nucleopolyhedrovirus genome.";
 RL Virology 294:106-121(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=90/2;
 RA Li Q., Donly C., Li L., Willis L.G., Theilmann D.A., Erlandson M.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U59461; AM09152.1; -; Genomic_DNA.
 DR InterPro; IPR011568; Viral_DUF.
 DR ProDom; PD021627; Viral_DUF; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 173 AA; 20238 MW; F85DFDAA70912360 CRC64;
 Query Match 51.7%; Score 46; DB 2; Length 173;
 Best Local Similarity 54.5%; Pred. No. 67;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VLCWTWETCER 13
 DB 146 VRCWVWGLCEK 156
 RESULT 20
 OS Q8JMB3_9NUCL
 ID Q8JMB3_9NUCL PRELIMINARY; PRT; 175 AA.
 AC Q8JMB3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 OS Mamestra configurata nucleopolyhedrovirus B.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=204440;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22080411; PubMed=12083822; DOI=10.1006/viro.2002.1411;
 RA Li L., Donly C., Li Q., Willis L.G., Keddle B.A., Erlandson M.A.,
 RA Theilmann D.A.;
 RT "Identification and genomic analysis of a second species of
 RT nucleopolyhedrovirus isolated from Mamestra configurata.";
 RL Virology 297:236-244(2002).
 DR EMBL; AY126275; AM95026.1; -; Genomic_DNA.
 DR InterPro; IPR011568; Viral_DUF.
 DR ProDom; PD021627; Viral_DUF; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 175 AA; 20193 MW; 8999CC171B8313C7 CRC64;
 Query Match 51.7%; Score 46; DB 2; Length 175;
 Best Local Similarity 54.5%; Pred. No. 68;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 3 VLCWTWETCER 13
 DB 148 VRCWVWGLCEK 158
 RESULT 21
 OS Q71AG8_9NUCL
 ID Q71AG8_9NUCL PRELIMINARY; PRT; 232 AA.
 AC Q71AG8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Mamestra configurata nucleopolyhedrovirus A.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=207830;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=90/4;
 RX PubMed=15604435; DOI=10.1099/vir.0.80488-0;
 RA Li L., Li Q., Willis L.G., Erlandson M., Theilmann D.A., Donly C.;
 RT "Complete comparative genomic analysis of two field isolates of
 RT Mamestra configurata nucleopolyhedrovirus-A.";
 RL J. Gen. Virol. 86:91-105(2005).

```

DR EMBL; AF539999; RAQ11063.1; -; Genomic_DNA.
DR InterPro; IPR011568; Viral_DUF.
DR ProDom; PD021627; Viral_DUF; 1.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 26958 MW; 9D4302AE6BC39B1B CRC64;

Query Match 51.7%; Score 46; DB 2; Length 232;
Best Local Similarity 54.5%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 VLCTWTETCE 13
Db 205 VRCWVGLCEK 215

RESULT 22
Q5UPF0 MIMIV
ID Q5UPF0 MIMIV PRELIMINARY; PRT; 232 AA.
AC Q5UPF0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MIMI_R73;
OS Mimivirus.
OC Viruses; dsDNA viruses, no RNA stage; Mimivirus.
OX NCBI_TaxID=212035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX MEDLINE=22550848; PubMed=12663918; DOI=10.1126/science.1081867;
RA La Scola B., Audic S., Robert C., Jungang L., de Lamballerie X.,
RA Drancourt M., Birtles R., Claverie J.M., Raoult D.;
RT "A giant virus in amoebae.";
RL Science 299:2033-2033(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Rowbotham-Bradford;
RX PubMed=15486256; DOI=10.1126/science.1101485;
RA Raoult D., Audic S., Robert C., Abergel C., Renesto P., Ogata H.,
RA La Scola B., Susan M., Claverie J.M.;
RT "The 1.2-Mb Genome Sequence of Mimivirus.";
RL Science 306:1344-1350(2004).
DR EMBL; AY653733; AAV50348.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 232 AA; 27261 MW; 550B66AC16756362 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 232;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCE 12
Db 42 EPHYCWTFTWCE 52

RESULT 23
Q4X1V6 ASPFU
ID Q4X1V6 ASPFU PRELIMINARY; PRT; 274 AA.
AC Q4X1V6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu2G08630;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,

Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
Penalva M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,
Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
White O., Woodward J., Yu J.-H., Frazer C., Galagan J.E., Asai K.,
Machida M., Hall N., Barrell B., Denning D.W.;
"Genomic sequence of the pathogenic and allergenic filamentous fungus
Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DDJB databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AAHF01000001; EAL93159.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 274 AA; 30852 MW; 516218FABA61B5AE CRC64;

Query Match 51.7%; Score 46; DB 2; Length 274;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCTWT 8
Db 198 WDVLYWTW 205

RESULT 24
Q7B3G3 CLOTM
ID Q7B3G3 CLOTM PRELIMINARY; PRT; 315 AA.
AC Q7B3G3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) (Fragment).
GN Name=cbhA;
OS Clostridium thermocellum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=F7;
RX MEDLINE=99351130; PubMed=10422230; DOI=10.1007/s002530051473;
RA Zverlov V.V., Velikodvorskaya G.A., Schwarz W.H.;
RT "Duplicated Clostridium thermocellum cellobiohydrolase gene encoding
cellulosomal subunits S3 and S.";
RL Appl. Microbiol. Biotechnol. 51:852-859(1999).
DR EMBL; AJ005783; CAA06693.1; -; Genomic_DNA.
DR GO; GO:0008810; F:cellulase activity; IEA.
DR GO; GO:0016162; F:cellulose 1,4-beta-cellobiosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR003305; CBM_CenC.
DR InterPro; IPR004197; Glyco_hydro_91g.
DR Pfam; PF02018; CBM 4_9; 1.
DR Pfam; PF02927; CelD_N; 1.
KW Glycosidase; Hydrolase.
FT NON_TER 315
SQ SEQUENCE 315 AA; 35887 MW; 55148EC06413ADC0 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 315;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;

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Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLQWETCE 12
| | | | |
DB 50 EGLCYPWHTCE 60

RESULT 25

O74498 SCHPO PRELIMINARY; PRT; 427 AA.
AC O74498;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SPCC285.11 protein.
GN ORFNames=SPCC285.11;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Ruckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson S., Saunders D., Seeger K., Sharp S.,
RA Rutherford J.K., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Skelton T., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volkert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoet A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Gadiou E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovskiy G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
DR EMBL; AL031545; CAA20850.1; -; Genomic_DNA.
DR PIR; T41257; T41257.
DR GeneDB Spombe; SPCC285.11; -.
DR InterPro; IPR006577; UAS.
DR InterPro; IPR001012; UBX.
DR Pfam; PF00789; UBX; 1.
DR SMART; SM00594; UAS; 1.
DR SMART; SM00166; UBX; 1.
DR PROSITE; PS0033; UBX; 1.
KW Complete proteome.

SQ SEQUENCE 427 AA; 48670 MW; 3AA7E161BELF7D90 CRC64;
Query Match 51.7%; Score 46; DB 2; Length 427;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLCWETCE 12
: | | | : | |
DB 178 ILCWTGDVCE 187

RESULT 26

O4WQ46 ASPFU PRELIMINARY; PRT; 564 AA.
AC O4WQ46;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Glycerol kinase, putative.
GN ORFNames=Afu4G11540;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nieman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Kellier N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penava M.A., Petea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC -!- SIMILARITY: Belongs to the FGXY kinase family.
CC EMBL; AAHF01000005; EA89638.1; -; Genomic_DNA.
DR InterPro; IPR000577; FGXY_kin.
DR InterPro; IPR005999; Glycerol_kin.
DR Pfam; PF02782; FGXY_C; 1.
DR Pfam; PF00370; FGXY_N; 1.
DR TIGRFAMs; TIGR01311; glycerol_kin; 1.
DR PROSITE; PS00445; FGXY_KINASES_2; 1.
KW Kinase; Transferase.
SQ SEQUENCE 564 AA; 62259 MW; 69C38809ED90F28A CRC64;

Query Match 51.7%; Score 46; DB 2; Length 564;
Best Local Similarity 77.8%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LCWETWETCE 12
| | | | |
DB 135 LCWDETGE 143

RESULT 27

O9GRV9 CAEEL PRELIMINARY; PRT; 1042 AA.
AC O9GRV9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein pcp-4.
GN Name=pcp-4; ORFNames=Y16P11B.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;

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RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Bristol N2;
RA Sulston J.E., McIay K.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBSJ databases.
RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AL132943; CAC14390.1; -; Genomic DNA.
DR Ensembl; Y116F11B.3; Caenorhabditis elegans.
DR WormBase; WBGene00003959; pcp-4.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008758; Peptidase_S28.
DR Pfam; PF05577; Peptidase_S28; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1042 AA; 116389 MW; FCD2A79BD7359B60 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 1042;
Best Local Similarity 75.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
DB 854 LLWTWQTC 861

RESULT 28
ID O01979 CAEEL PRELIMINARY; PRT; 1080 AA.
AC O01979_002253;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein pcp-2.
GN Name=pcp-2; ORFNames=F23B2.12;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).
DR EMBL; 282266; CA905187.1; -; Genomic DNA.
DR EMBL; 268295; CA92588.1; -; Genomic DNA.
DR EMBL; 268295; CA905187.1; JOINED; Genomic DNA.
DR EMBL; 282266; CA92588.1; JOINED; Genomic DNA.
DR PIR; T19048; T19048.
DR Ensembl; F23B2.12; Caenorhabditis elegans.
DR WormBase; WBGene00003957; pcp-2.
DR WormPep; F23B2.12; C809592.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008758; Peptidase_S28.
DR InterPro; IPR000379; Ser_estrs-
DR Pfam; PF05577; Peptidase_S28; 2.
KW Complete proteome; Hydroxylase; Hypothetical protein; Lysosome;
  Protease.
SQ SEQUENCE 1080 AA; 121536 MW; C34B6E5D19BA7782 CRC64;

Query Match 51.7%; Score 46; DB 2; Length 1080;

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Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
DB 886 LLWTWQTC 893

RESULT 29
ID Q60QJ5 CAEER PRELIMINARY; PRT; 1085 AA.
AC Q60QJ5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG21793 (Fragment).
GN Name=CBG21793;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
  preliminary data.
DR EMBL; CAC01000124; CAE74127.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008236; F:serine-type peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008758; Peptidase_S28.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF05577; Peptidase_S28; 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 1085 AA; 121617 MW; D5836B7B41C5629D CRC64;

Query Match 51.7%; Score 46; DB 2; Length 1085;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
DB 890 LLWTWQTC 897

RESULT 30
ID O02252 CAEEL PRELIMINARY; PRT; 1121 AA.
AC O02252;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein pcp-3.
GN Name=pcp-3; ORFNames=F23B2.11;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).
DR EMBL; 282266; CA905185.1; -; Genomic DNA.
DR PIR; T21303; T21303.
DR Ensembl; F23B2.11; Caenorhabditis elegans.

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DR WormBase; WBGene0003958; pcp-3.
 DR WormBep; F23B2.11; CR09591.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008758; Peptidase_S28.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF05577; Peptidase_S28; 2.
 DR Complete proteome; Hydrolase; Hypothetical protein; Lysosome;
 KW Protease.
 SQ SEQUENCE 1121 AA; 125951 MW; A1B4D7BD92116E85 CRC64;
 Query Match 51.7%; Score 46; DB 2; Length 1121;
 Best Local Similarity 75.0%; Pred. No. 4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LCWTWETC 11
 DB 928 LLWTWQTC 935

RESULT 31
 Q59325_CLOTH
 ID Q59325 CLOTH PRELIMINARY; PRT; 1230 AA.
 AC Q59325;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91).
 GN Name=cbaH;
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=E7;
 RA Zverlov V.V., Velikodvorskaya G.V., Schwarz W.H., Bronnenmeier K.,
 RA Kellermann J., Staudenbauer W.L.;
 RT "Multidomain structure and cellobiosomal localization of the
 RT Clostridium thermocellum cellobiohydrolase CbaH";
 RL J. Bacteriol. 180:3091-3099(1998).
 DR EMBL; X80993; CAA56918.1; -; Genomic_DNA.
 DR PIR; S47466; S47466.
 DR PDB; 1RQ5; X-ray; A=208-818.
 DR PDB; 1UT9; X-ray; A=-.
 DR GO; GO:0008810; F:cellulase activity; IEA.
 DR GO; GO:0016162; F:cellulose 1,4-beta-cellobiosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0030245; P:cellulose catabolism; IEA.
 DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
 DR InterPro; IPR001956; CBD_3.
 DR InterPro; IPR003305; CBM_Cent.
 DR InterPro; IPR002105; Dockerin_1.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001701; Glyco_hydro_9.
 DR InterPro; IPR004197; Glyco_hydro_919.
 DR Pfam; PF0942; CBM_3; 1.
 DR Pfam; PF02018; CBM_4; 9; 1.
 DR Pfam; PF02927; Celd_N; 1.
 DR Pfam; PF00404; Dockerin_1; 2.
 DR Pfam; PF00759; Glyco_hydro_9; 1.
 DR ProDom; PD001947; CBD_3; 1.
 DR PROSITE; PS00448; CLOS_CELLULOSE_RPT; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
 DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; UNKNOWN_1.
 DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 1230 AA; 138077 MW; A398D9814B5D6A0E CRC64;

Query Match 51.7%; Score 46; DB 2; Length 1230;
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCE 12
 DB 50 EGLCYPWHICE 60

RESULT 32
 Q86P30_DROME
 ID Q86P30 DROME PRELIMINARY; PRT; 807 AA.
 AC Q86P30;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE RE34115P.
 GN ORFNames=CG15236;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT003507; AAO39511.1; -; mRNA.
 DR Ensembl; CG15236; Drosophila melanogaster.
 DR FlyBase; FBgn0033108; CG15236.
 SQ SEQUENCE 807 AA; 87694 MW; 6B4BDB067BA4BDF7 CRC64;

Query Match 51.1%; Score 45.5; DB 2; Length 807;
 Best Local Similarity 50.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 EVLCWTWETCER 13
 DB 161 EIFCW-WEKCDK 171

RESULT 33
 Q9V995_DROME
 ID Q9V995 DROME PRELIMINARY; PRT; 807 AA.
 AC Q9V995;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG15236-PA, isoform A (CG15236-pb, isoform b).
 GN Name=CG15236; ORFNames=CG15236;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Richards S., Ashburner M., Henderson S.N.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RN Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupay J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION:

CC Q9VTB3:CG11811; NBExp=1; Intact=EBI-163727, EBI-106486;
DR EMBL; AE003790; AAM70834.1; -; Genomic_DNA.
DR Intact; Q9V995; -;
DR Ensembl; CG15236; *Drosophila melanogaster*.
DR FlyBase; FBgn0033108; CG15236. 798C5EC7IA5162D0 CRC64;
SQ SEQUENCE 807 AA; 87622 MW; 798C5EC7IA5162D0 CRC64;
Query Match 51.1%; Score 45.5; DB 2; Length 807;
Best Local Similarity 50.0%; Pred. NO. 3.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
QY 2 EVLCWTWETCER 13
Db 161 BIFCW-WEKCDK 171
RESULT 34
Q8N8D9 HUMAN PRELIMINARY; ID Q8N8D9 HUMAN PRELIMINARY; PRT; 126 AA.
AC Q8N8D9;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Hypothetical protein FLJ39622.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hoshiro T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T.,
RA Kusanagi J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togawa S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK036941; BAC04907.1; -; mRNA.
DR Ensembl; ENSG00000197536; Homo sapiens.
SQ SEQUENCE 126 AA; 14682 MW; BBF1A87EAD306AB6 CRC64;
Query Match 50.6%; Score 45; DB 2; Length 126;
Best Local Similarity 62.5%; Pred. NO. 69;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 LCWTWETC 11


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Db      98 LCWAWQC 105
|||||
RESULT 35
ID 087830 STRAT PRELIMINARY; PRT; 426 AA.
AC 087830;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glycosyltransferase.
GN Name=olegi;
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1890;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 11891;
RC MEDLINE=98420102; PubMed=9749673; DOI=10.1007/s004380050816;
RA Olano C., Rodriguez A.M., Michel J.M., Mendez C., Raynal M.C.,
RA Salas J.A.;
RT Analysis of a Streptomyces antibiotic chromosomal region involved
RT in oleandomycin biosynthesis, which encodes two glycosyltransferases
RT responsible for glycosylation of the macrolactone ring."
RL Mol. Gen. Genet. 259:299-308(1998).
DR EMBL: AJ002638; CAA05641.1; -, Genomic_DNA.
DR GO: 0016740; F:transferase activity; IEA.
DR GO: 0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO: 0005975; P:carbohydrate metabolism; IEA.
DR GO: 0030259; P:lipid glycosylation; IEA.
DR InterPro: IPR010610; DUF1205.
DR InterPro: IPR004276; Glyco_trans_28.
DR Pfam: PF06722; DUF1205; 1.
DR Pfam: PF03033; Glyco_transf_28; 1.
KW Transferase.
SQ SEQUENCE 426 AA; 47008 MW; 4BADDD0551BC25EC CRC64;

Query Match 50.6%; Score 45; DB 2; Length 426;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 WTWETCER 13
|||||
DB 239 WWPCEP 246

RESULT 36
ID Q5PNM8 BRARE PRELIMINARY; PRT; 481 AA.
AC Q5PNM8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein.
GN ORFNames=DKEY-204F11.59-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Calcium-dependent mitochondrial aspartate and glutamate
CC carrier. May have a function in the urea cycle (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC EMBL: BX649502; CAC20828.1; -, Genomic_DNA.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0005743; C:mitochondrial inner membrane; IEA.

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DR GO: 0005739; C:mitochondrion; IEA.
DR GO: 0005488; F:binding; IEA.
DR GO: 0005509; F:calcium ion binding; IEA.
DR GO: 0005215; F:transporter activity; IEA.
DR GO: 0006810; P:transport; IEA.
DR InterPro: IPR002113; Aden_tnsclotr.
DR InterPro: IPR002048; EF_Hand_Ca_bd.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PRINTS: PR00926; MITOCARRIER.
DR ProDom: PD000012; EF-hand; 2.
DR SMART: SMO0054; EFh; 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_3.
DR PROSITE: PS00920; SOLCAR; 3.
DR Calcium; Inner membrane; Mitochondrion; Repeat; Transmembrane;
KW Transport.
SQ SEQUENCE 481 AA; 53776 MW; FCECAD7D1ACB1041 CRC64;

Query Match 50.6%; Score 45; DB 2; Length 481;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 CWTWETCE 12
|||||
DB 11 CWTWARCQ 18

RESULT 37
ID Q4Q987 LEIMA PRELIMINARY; PRT; 513 AA.
AC Q4Q987;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF26.1070;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CT005265; CAJ05084.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 513 AA; 54750 MW; 18C611C93A14C07B CRC64;

Query Match 50.6%; Score 45; DB 2; Length 513;
Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLWETWETCER 13
|:::|
DB 233 WDTMCTTWEAMR 245.

RESULT 38
ID Q4WLK9 ASPFU PRELIMINARY; PRT; 514 AA.
AC Q4WLK9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine/threonine protein kinase, putative.
GN ORFNames=Afu6g13160;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

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OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AF293;
 RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
 RA Artzy J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman H.H., Gomi K., Griffith-Jones S., Guilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Penvalva M.A., Pettea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT Aspergillus fumigatus";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AAH0100006; EAL89155.1; -: Genomic_DNA.
 KW Kinase; Serine/threonine-protein kinase.
 SQ SEQUENCE 514 AA; 57848 MW; BF6F894A358DB9355 CRC64;
 Query Match 50.6%; Score 45; DB 2; Length 514;
 Best Local Similarity 75.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 VLCWTWET 10
 DB 492 VLCWLWDT 499
 RESULT 39
 ID Q5L1D4_GEOKA PRELIMINARY; PRT; 673 AA.
 AC Q5L1D4;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Acylaminoacyl-peptidase (EC 3.4.19.1).
 GN OrderedLocustNames=GK0961;
 OS Geobacillus kaustophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTA426;
 RX PubMed=15576355; DOI=10.1093/nar/gkh970;
 RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
 RA Matsui S., Uchiyama I.;
 RT "Thermoadaptation trait revealed by the genome sequence of
 RT thermophilic Geobacillus kaustophilus";
 RL Nucleic Acids Res. 32:6292-6303(2004).
 DR EMBL: BA000043; BAD75246.1; -: Genomic DNA.
 DR GO: GO:0004254; F:acylaminoacyl-peptidase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0008236; F:serine-type peptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR011659; PD40.
 DR InterPro: IPR001375; Peptidase S9.
 DR InterPro: IPR000379; Ser_estra-
 PFam: PF07676; PD40; 3.

DR Pfam: PF00326; Peptidase S9; 1.
 KW Complete proteome: Hydrolase.
 SQ SEQUENCE 673 AA; 75440 MW; C40384EB090CFF11 CRC64;
 Query Match 50.6%; Score 45; DB 2; Length 673;
 Best Local Similarity 61.5%; Pred. No. 3.4e+02;
 Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 1 WEVLCWTWETCER 13
 DB 573 WEVGCDIWEADAER 585
 RESULT 40
 ID Q8A2Z2_BACTN PRELIMINARY; PRT; 674 AA.
 AC Q8A2Z2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-glucosidase, putative.
 GN OrderedLocustNames=Bf3163;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";
 RL Science 299:2074-2076(2003).
 DR EMBL: AE016939; AAO78269.1; -: Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 674 AA; 77744 MW; BFE4E91596D14C97 CRC64;
 Query Match 50.6%; Score 45; DB 2; Length 674;
 Best Local Similarity 41.7%; Pred. No. 3.4e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 2 EVLCWTWETCER 13
 DB 390 KIIVWTWASCAR 401
 RESULT 41
 ID O68438_CLOTM PRELIMINARY; PRT; 895 AA.
 AC O68438;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91).
 GN Name=celK;
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JW 20;
 RX MEDLINE=99395035; PubMed=10464199;
 RA Kataeva I., Li X.-L., Chen H., Choi S.K., Ljungdahl L.G.;
 RT "Cloning and sequence analysis of a new cellulase gene encoding CelK,
 RT a major cellulosome component of Clostridium thermocellum: evidence
 RT for gene duplication and recombination";
 RL J. Bacteriol. 181:5288-5295(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JW 20;
 RA Kataeva I.A., Li X.-L., Chen H.Z., Choi S.-K., Ljungdahl L.G.;

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RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039030; AAC06139.1; -; Genomic_DNA.
DR HSSP; P38686; 1DAV.
DR SMR; O68438; 831-895.
DR GO; GO:000810; F:cellulase activity; IEA.
DR GO; GO:0016162; F:cellulose 1,4-beta-cellobiosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030245; P:cellulose catabolism; IEA.
DR GO; GO:000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR003305; CBM Cenc.
DR InterPro; IPR002105; Dockerin_1.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001701; Glyco_hydro_9.
DR InterPro; IPR004197; Glyco_hydro_9ig.
DR Pfam; PF02018; CBM 4_9; 1.
DR Pfam; PF02927; CelD_N; 1.
DR Pfam; PF00404; Dockerin_1; 2.
DR Pfam; PF00759; Glyco_hydro_9; 1.
DR PROSITE; PS00448; CLOS_CELLULOSE_RPT; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; UNKNOWN_1.
DR PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 895 AA; 100711 MW; 5DB1FD846750CCB CRC64;

Query Match 50.6%; Score 45; DB 2; Length 895;
Best Local Similarity 63.6%; Pred. No. 4.5e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCTWETCE 12
DB 50 EGLCPFWHTCE 60
|||||

RESULT 42
QSR549 PONPY PRELIMINARY; PRT; 59 AA.
AC QSR549;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp470N0914.
GN Name=DKFp470N0914;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Liver;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR861023; CAH93117.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 59 AA; 6034 MW; E3399AB917F1D8B CRC64;

Query Match 49.4%; Score 44; DB 2; Length 59;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLCTWETCE 13
DB 8 LLCWACSTCDR 18
|||||

RESULT 43
Q8TNM4_METAC PRELIMINARY; PRT; 155 AA.
AC Q8TNM4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocustNames=MA2260;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1193238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Linton N., Naylor J., Stange-Thomann N., DeAtellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Rederich R., Ingram-Smith C., Kuettnar H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AF010913; AAM05654.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 155 AA; 17660 MW; F0052FD95AD5D5F5 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 155;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 WEVLCTWETCE 13
DB 105 WE--CGTETCEK 115
|||||

RESULT 44
Q9DFQ6_GILMI PRELIMINARY; PRT; 168 AA.
AC Q9DFQ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 60S ribosomal protein L6 (Fragment).
OS Gillichthys mirabilis (Long-jawed mudsucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae;
OC Gobiidae; Gillichthys.
OX NCBI_TaxID=8222;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Liver;
RX MEDLINE=21117151; PubMed=11172064; DOI=10.1073/pnas.98.4.1993;
RA Gracey A.Y., Troll J.V., Somero G.N.;
RT "Hypoxia-induced gene expression profiling in the euryoxic fish
RT Gillichthys mirabilis."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
DR EMBL; AF266176; AAG13296.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000915; Ribosomal_L6E.
DR InterPro; IPR005568; Ribosomal_L6E_N.
DR Pfam; PF03869; Ribosomal_L6E_N_1.
DR ProDom; PD009612; Ribosomal_L6E; 1.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 168
FT NON_TER 168

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SQ SEQUENCE 168 AA; 19385 MW; E2584EC0F22C3504 CRC64;
Query Match 49.4%; Score 44; DB 2; Length 168;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLCTWETC 11
Db 143 VCCSWPSC 151

RESULT 45
Q5B307 EMENI PRELIMINARY; PRT; 240 AA.
AC Q5B307;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Predicted protein.
GN ORFNames=AN5073.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutriales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Gardyna S., Gnerre S., Graham L., Fitzgerald M., Gage D., Galagan J.,
RA Hagoopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihoava T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RA "Fusarium graminearum genome sequence.";
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC001000442; EAA68438.1; -; Genomic DNA.
SQ SEQUENCE 272 AA; 30601 MW; ADE81DF89DF3FF65 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 272;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLCTWETC 12
Db 32 VLNNWELCE 41

RESULT 47
Q7VRB2 CANBF PRELIMINARY; PRT; 320 AA.
AC Q7VRB2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative membrane protein.
GN Name-yctf; OrderedLocNames=Bfl307;
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22784745; PubMed=12886019; DOI=10.1073/pnas.1533499100;
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Latorre A., Russell C., Kamerbeek J., Gadau J., Hoelldobler B.,
RA van Ham R.C.H.J., Gross R., Moya A.;
RT "The genome sequence of Blochmannia floridanus: comparative analysis
RT of reduced genomes";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
DR EMBL; BX248585; CAD83377.1; -; Genomic DNA.
KW Complete proteome.
SQ SEQUENCE 320 AA; 36384 MW; 9944DBABE9809BB4 CRC64;
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SQ SEQUENCE 168 AA; 19385 MW; E2584EC0F22C3504 CRC64;
Query Match 49.4%; Score 44; DB 2; Length 168;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLCTWETC 11
Db 143 VCCSWPSC 151

RESULT 45
Q5B307 EMENI PRELIMINARY; PRT; 240 AA.
AC Q5B307;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Predicted protein.
GN ORFNames=AN5073.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutriales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Gardyna S., Gnerre S., Graham L., Fitzgerald M., Gage D., Galagan J.,
RA Hagoopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihoava T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RA "Genome Sequence of Aspergillus nidulans.";
RT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC001000086; EAA60168.1; -; Genomic DNA.
SQ SEQUENCE 240 AA; 27238 MW; 0E1A6D64A7B34FC8 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 240;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEVLCTWET 10
Db 39 WEQLVWEWES 48

RESULT 46
Q4HWV6 GIBZE PRELIMINARY; PRT; 272 AA.
AC Q4HWV6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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Query Match 49.4%; Score 44; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLCWTW 8
DB 171 VLCWTW 176
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RESULT 48
Q8TVTS METKA
ID Q8TVTS_METKA PRELIMINARY; PRT; 350 AA.
AC Q8TVTS;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Uncharacterized domain specific for M.kandleri, MK-11 family.
GN OrderedLocusNames=MK1303;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OC NCBI_TaxID=2320;
RX NCBI_TaxID=2320;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=2197647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natalie D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malysk A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AB010422; AM02516.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 350 AA; 39026 MW; 687FC75CE4507E38 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 350;
Best Local Similarity 75.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
DB 128 WKVLCWTW 135
|||||

RESULT 49
Q60VV2 CAEBR
ID Q60VV2_CAEBR PRELIMINARY; PRT; 360 AA.
AC Q60VV2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG19383.
GN Names=CBG19383;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000098; CAE72264.1; -; Genomic_DNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0004930; F.G-protein coupled receptor activity; IEA.
DR InterPro; IPR003002; 7TM_chemrecept1.
DR InterPro; IPR000168; Nm7TM_chemrecept.
DR Pfam; PF01461; 7tm_4; 1.

KW Hypothetical protein.
SQ SEQUENCE 360 AA; 41246 MW; 47D731713A5A545F CRC64;

Query Match 49.4%; Score 44; DB 2; Length 360;
Best Local Similarity 46.7%; Pred. No. 2.6e+02; Indels 2; Gaps 1;
Matches 7; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 WEVLCWTW--ETCER 13
DB 148 WGIICWVYGETSER 162
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RESULT 50
Q57XP3 9TRYP
ID Q57XP3_9TRYP PRELIMINARY; PRT; 421 AA.
AC Q57XP3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE DNA primase small subunit, putative (EC 2.7.7.-).
GN ORFNames=TB927.7.2310;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GUTat10.1;
RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,
RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,
RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,
RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,
RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC159413; AAX69626.1; -; Genomic_DNA.
DR GO; GO:0005658; C.alpha DNA polymerase:primase complex; IEA.
DR GO; GO:0003896; F:DNA primase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006269; P:DNA replication, synthesis of RNA primer; IEA.
KW DNA replication; DNA-directed RNA polymerase; Nucleotidyltransferase;
KW Primosome; Transferase.
SQ SEQUENCE 421 AA; 47893 MW; E6C5BC76CFB4CE68 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 3e+02; Indels 1; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 CWTWETC 11
DB 162 CWTWMSC 168
|||||

Search completed: March 28, 2006, 11:51:08
Job time : 273 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:51:25 / Search time 47 Seconds
(without alignments)
22.868 Million cell updates/sec

Title: US-10-639-076-4

Perfect score: 89

Sequence: 1 WEVLQWTWCER 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	52.8	54	2	US-09-621-976-5389
2	47	52.8	54	2	US-09-621-976-5390
3	46	51.7	407	2	US-09-352-991A-29811
4	45.5	51.1	126	2	US-09-949-016-10235
5	45.5	51.1	169	2	US-09-270-767-40967
6	45.5	51.1	169	2	US-09-702-705-1818
7	44	49.4	102	2	US-09-736-457-1818
8	44	49.4	102	2	US-09-671-325-1818
9	44	49.4	102	2	US-10-017-754-1818
10	44	49.4	216	2	US-09-252-991A-23048
11	44	49.4	257	2	US-09-252-991A-31868
12	44	49.4	13	2	US-10-158-847-101
13	43.5	48.9	13	2	US-10-158-825-101
14	43.5	48.9	13	2	US-10-158-847-30
15	43.5	48.9	21	2	US-10-158-847-30
16	43.5	48.9	21	2	US-10-158-825-30
17	43	48.3	54	2	US-08-851-843A-183
18	43	48.3	54	2	US-08-974-549A-302
19	43	48.3	54	2	US-08-854-050-183
20	43	48.3	54	2	US-09-430-323-183
21	43	48.3	54	2	US-09-402-181B-302
22	43	48.3	54	2	US-09-721-456-302
23	43	48.3	54	2	US-10-054-295-183
24	43	48.3	54	2	US-09-438-486A-183
25	43	48.3	227	2	US-09-352-991A-30379
26	43	48.3	458	2	US-09-922-364A-4
27	43	48.3	458	2	US-09-254-590-4

28	43	48.3	458	2	US-10-115-415-4	Sequence 4, Appli
29	43	48.3	458	2	US-10-116-260-4	Sequence 4, Appli
30	43	48.3	458	2	US-10-115-671-4	Sequence 4, Appli
31	43	48.3	458	2	US-10-115-695-4	Sequence 4, Appli
32	42	47.2	13	2	US-10-158-847-103	Sequence 103, App
33	42	47.2	13	2	US-10-158-825-103	Sequence 103, App
34	42	47.2	328	2	US-09-922-364A-27	Sequence 27, Appl
35	42	47.2	328	2	US-09-254-590-27	Sequence 27, Appl
36	42	47.2	328	2	US-10-115-415-27	Sequence 27, Appl
37	42	47.2	328	2	US-10-116-260-27	Sequence 27, Appl
38	42	47.2	328	2	US-10-115-671-27	Sequence 27, Appl
39	42	47.2	328	2	US-10-115-695-27	Sequence 27, Appl
40	42	47.2	386	2	US-09-949-016-10095	Sequence 10095, A
41	42	47.2	553	2	US-09-922-364A-3	Sequence 3, Appli
42	42	47.2	553	2	US-09-254-590-3	Sequence 3, Appli
43	42	47.2	553	2	US-10-115-415-3	Sequence 3, Appli
44	42	47.2	553	2	US-10-116-260-3	Sequence 3, Appli
45	42	47.2	553	2	US-10-115-671-3	Sequence 3, Appli
46	42	47.2	553	2	US-10-115-695-3	Sequence 3, Appli
47	42	47.2	557	2	US-09-922-364A-20	Sequence 20, Appl
48	42	47.2	557	2	US-09-254-590-20	Sequence 20, Appl
49	42	47.2	557	2	US-10-115-415-20	Sequence 20, Appl
50	42	47.2	557	2	US-10-116-260-20	Sequence 20, Appl
51	42	47.2	557	2	US-10-115-671-20	Sequence 20, Appl
52	42	47.2	557	2	US-10-115-695-20	Sequence 20, Appl
53	42	47.2	561	2	US-09-922-364A-1	Sequence 1, Appli
54	42	47.2	561	2	US-09-254-590-1	Sequence 1, Appli
55	42	47.2	561	2	US-09-949-016-6197	Sequence 6197, Ap
56	42	47.2	561	2	US-10-115-415-1	Sequence 1, Appli
57	42	47.2	561	2	US-10-116-260-1	Sequence 1, Appli
58	42	47.2	561	2	US-10-115-671-1	Sequence 1, Appli
59	42	47.2	561	2	US-10-115-695-1	Sequence 1, Appli
60	42	47.2	579	2	US-09-922-364A-19	Sequence 19, Appl
61	42	47.2	579	2	US-09-254-590-19	Sequence 19, Appl
62	42	47.2	579	2	US-10-115-415-19	Sequence 19, Appl
63	42	47.2	579	2	US-10-116-260-19	Sequence 19, Appl
64	42	47.2	579	2	US-10-115-671-19	Sequence 19, Appl
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67	42	47.2	580	2	US-09-254-590-2	Sequence 2, Appli
68	42	47.2	580	2	US-10-115-415-2	Sequence 2, Appli
69	42	47.2	580	2	US-10-116-260-2	Sequence 2, Appli
70	42	47.2	580	2	US-10-115-671-2	Sequence 2, Appli
71	42	47.2	580	2	US-10-115-695-2	Sequence 2, Appli
72	42	47.2	587	2	US-09-949-016-10091	Sequence 10091, A
73	42	47.2	712	2	US-09-252-991A-20471	Sequence 20471, A
74	42	47.2	731	2	US-09-115-446-2	Sequence 2, Appli
75	42	47.2	731	2	US-09-275-252A-10	Sequence 10, Appl
76	42	47.2	731	2	US-09-565-590-2	Sequence 2, Appli
77	42	47.2	732	2	US-09-922-364A-43	Sequence 43, Appl
78	42	47.2	732	2	US-09-254-590-43	Sequence 43, Appl
79	42	47.2	732	2	US-10-115-415-43	Sequence 43, Appl
80	42	47.2	732	2	US-10-116-260-43	Sequence 43, Appl
81	42	47.2	732	2	US-10-115-671-43	Sequence 43, Appl
82	42	47.2	732	2	US-10-115-695-43	Sequence 43, Appl
83	42	47.2	736	2	US-09-922-364A-47	Sequence 47, Appl
84	42	47.2	736	2	US-09-254-590-47	Sequence 47, Appl
85	42	47.2	736	2	US-10-115-415-47	Sequence 47, Appl
86	42	47.2	736	2	US-10-116-260-47	Sequence 47, Appl
87	42	47.2	736	2	US-10-115-671-47	Sequence 47, Appl
88	42	47.2	736	2	US-10-115-695-47	Sequence 47, Appl
89	42	47.2	829	2	US-09-949-016-7161	Sequence 7161, Ap
90	42	47.2	847	2	US-10-162-012-2	Sequence 2, Appli
91	41	46.1	87	2	US-09-270-767-43422	Sequence 43422, A
92	41	46.1	115	2	US-09-621-976-5517	Sequence 5517, Ap
93	41	46.1	172	2	US-09-270-767-60977	Sequence 60977, A
94	41	46.1	202	2	US-09-252-991A-20104	Sequence 20104, A
95	41	46.1	207	2	US-09-302-540-10098	Sequence 10098, A
96	41	46.1	231	2	US-09-914-098-6	Sequence 6, Appli
97	41	46.1	419	2	US-09-270-767-45469	Sequence 45469, A
98	41	46.1	526	2	US-09-252-991A-23688	Sequence 23688, A
99	41	46.1	615	2	US-09-602-787A-534	Sequence 534, App
100	41	46.1				

101	41	46.1	615	2	US-09-602-787A-536	Sequence 536, App	174	38	42.7	152	2	US-09-702-705-787	Sequence 787, App
102	40.5	45.5	4861	2	US-09-913-437-70	Sequence 70, Appl	175	38	42.7	152	2	US-09-702-705-795	Sequence 795, App
103	40	44.9	90	2	US-09-270-767-34477	Sequence 34477, A	176	38	42.7	152	2	US-09-736-457-787	Sequence 787, App
104	40	44.9	901	2	US-09-270-767-49694	Sequence 49694, A	177	38	42.7	152	2	US-09-736-457-795	Sequence 795, App
105	40	44.9	101	2	US-09-621-976-7733	Sequence 7733, Ap	178	38	42.7	152	2	US-09-614-124B-787	Sequence 787, App
106	40	44.9	102	2	US-09-270-767-40715	Sequence 40715, A	179	38	42.7	152	2	US-09-614-124B-795	Sequence 795, App
107	40	44.9	102	2	US-09-270-767-55931	Sequence 55931, A	180	38	42.7	152	2	US-09-671-325-787	Sequence 787, App
108	40	44.9	150	2	US-09-543-681A-7881	Sequence 7881, Ap	181	38	42.7	152	2	US-09-671-325-795	Sequence 795, App
109	40	44.9	280	2	US-09-712-363-216	Sequence 216, App	182	38	42.7	152	2	US-09-589-184-787	Sequence 787, App
110	40	44.9	409	2	US-09-252-991A-20236	Sequence 20236, A	183	38	42.7	152	2	US-09-589-184-795	Sequence 795, App
111	40	44.9	443	2	US-08-821-994-65	Sequence 65, Appl	184	38	42.7	152	2	US-09-658-824-787	Sequence 787, App
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114	40	44.9	866	2	US-09-022-636-10	Sequence 10, Appl	187	38	42.7	152	2	US-10-017-754-795	Sequence 795, App
115	40	44.9	866	2	US-08-978-773-4	Sequence 4, Appll	188	38	42.7	152	2	US-09-651-563-787	Sequence 787, App
116	40	44.9	866	2	US-09-022-253-10	Sequence 10, Appl	189	38	42.7	152	2	US-09-651-563-795	Sequence 795, App
117	40	44.9	866	2	US-09-022-260-10	Sequence 10, Appl	190	38	42.7	152	2	US-09-519-642-787	Sequence 787, App
118	40	44.9	866	2	US-09-022-259-10	Sequence 10, Appl	191	38	42.7	152	2	US-09-252-991A-19256	Sequence 19256, A
119	40	44.9	866	2	US-09-022-257-10	Sequence 10, Appl	192	38	42.7	179	1	US-08-481-956A-11	Sequence 11, Appl
120	40	44.9	866	2	US-09-549-679-10	Sequence 10, Appl	193	38	42.7	179	1	US-08-629-291A-11	Sequence 11, Appl
121	40	44.9	866	2	US-10-033-522-1	Sequence 1, Appll	194	38	42.7	179	2	US-08-658-335B-11	Sequence 11, Appl
122	40	44.9	866	2	US-09-949-002-403	Sequence 403, App	195	38	42.7	179	2	US-09-406-840-11	Sequence 28845, A
123	40	44.9	876	2	US-09-949-002-412	Sequence 412, App	196	38	42.7	187	2	US-09-252-991A-26845	Sequence 732, App
124	40	44.9	900	2	US-08-890-865A-4	Sequence 4, Appll	197	38	42.7	187	2	US-10-101-464A-732	Sequence 8, Appll
125	40	44.9	1088	2	US-09-949-016-8011	Sequence 8011, Ap	198	38	42.7	215	1	US-08-659-251-8	Sequence 8, Appll
126	39.5	44.4	18	2	US-08-825-852-79	Sequence 79, Appl	199	38	42.7	215	4	US-09-256-490-8	Sequence 8, Appll
127	39.5	44.4	18	2	US-09-025-888-80	Sequence 80, Appl	200	38	42.7	215	4	PCT-US96-11445-8	Sequence 2829, Ap
128	39.5	44.4	18	2	US-09-723-890-80	Sequence 80, Appl	201	38	42.7	228	2	US-10-104-047-2829	Sequence 41694, A
129	39.5	44.4	18	2	US-09-723-901-80	Sequence 80, Appl	202	38	42.7	233	2	US-09-270-767-41694	Sequence 3, Appll
130	39.5	44.4	18	2	US-09-723-547-80	Sequence 80, Appl	203	38	42.7	246	2	US-08-634-475-3	Sequence 3, Appll
131	39.5	44.4	18	2	US-09-724-127-80	Sequence 80, Appl	204	38	42.7	246	2	US-09-709-791-3	Sequence 60, Appl
132	39.5	44.4	18	2	US-09-723-931-80	Sequence 80, Appl	205	38	42.7	261	1	US-07-857-224B-60	Sequence 2, Appll
133	39.5	44.4	18	2	US-09-723-873-80	Sequence 80, Appl	206	38	42.7	262	2	US-08-634-475-2	Sequence 2, Appll
134	39.5	44.4	18	2	US-09-724-114-80	Sequence 80, Appl	207	38	42.7	262	2	US-09-709-791-2	Sequence 7078, Ap
135	39.5	44.4	18	2	US-09-723-913-80	Sequence 80, Appl	208	38	42.7	297	2	US-09-949-016-7078	Sequence 28842, A
136	39.5	44.4	18	2	US-09-723-912-80	Sequence 80, Appl	209	38	42.7	323	2	US-09-252-991A-28842	Sequence 2, Appll
137	39.5	44.4	18	2	US-09-724-085-80	Sequence 80, Appl	210	38	42.7	323	2	US-08-532-896-2	Sequence 19475, A
138	39.5	44.4	18	2	US-09-724-157-80	Sequence 80, Appl	211	38	42.7	374	2	US-09-252-991A-19475	Sequence 902, App
139	39.5	44.4	18	2	US-09-724-062-80	Sequence 80, Appl	212	38	42.7	386	2	US-10-101-464A-902	Sequence 28430, A
140	39.5	44.4	18	2	US-09-724-065-80	Sequence 80, Appl	213	38	42.7	453	2	US-09-252-991A-24830	Sequence 8, Appll
141	39.5	44.4	18	2	US-09-724-481-80	Sequence 80, Appl	214	38	42.7	481	2	US-09-817-785-8	Sequence 8, Appll
142	39.5	44.4	117	2	US-09-270-767-47400	Sequence 47400, A	215	38	42.7	481	2	US-09-817-785-4	Sequence 4, Appll
143	39.5	44.4	196	2	US-09-252-991A-23657	Sequence 23657, A	216	38	42.7	867	2	US-09-817-785-4	Sequence 4, Appll
144	39.5	44.4	554	2	US-09-252-991A-28232	Sequence 28232, A	217	38	42.7	867	2	US-08-453-862-2	Sequence 2, Appll
145	39	43.8	13	2	US-10-158-847-112	Sequence 112, App	218	38	42.7	915	1	US-08-452-734A-2	Sequence 12, Appl
146	39	43.8	13	2	US-10-158-825-112	Sequence 112, App	219	38	42.7	915	2	US-08-176-401B-2	Sequence 2, Appll
147	39	43.8	64	2	US-10-178-213-299	Sequence 299, App	220	38	42.7	915	2	US-09-817-464-12	Sequence 12, Appl
148	39	43.8	135	2	US-09-252-991A-24701	Sequence 24701, A	221	38	42.7	915	4	PCT-US94-14989-2	Sequence 2, Appll
149	39	43.8	265	2	US-09-949-016-9336	Sequence 9336, Ap	222	38	42.7	915	2	US-08-617-785-14	Sequence 14, Appl
150	39	43.8	296	2	US-09-328-352-7482	Sequence 7482, Ap	223	38	42.7	922	2	US-09-817-464-14	Sequence 14, Appl
151	39	43.8	311	2	US-09-489-039A-13013	Sequence 13013, A	224	38	42.7	1402	2	US-09-711-619-9	Sequence 9, Appll
152	39	43.8	323	2	US-09-252-991A-22747	Sequence 22747, A	225	38	42.7	3077	6	5223423-2	Patent No. 5223423
153	39	43.8	340	2	US-09-712-368-1	Sequence 1, Appll	226	38	42.7	3077	6	5223423-2	Patent No. 5223423
154	39	43.8	340	2	US-10-314-048A-40	Sequence 40, Appl	227	38	42.7	3077	6	5223423-2	Patent No. 5223423
155	39	43.8	341	2	US-09-328-352-6124	Sequence 6124, Ap	228	37.5	42.1	13	2	US-10-158-847-118	Sequence 118, App
156	39	43.8	361	2	US-09-543-681A-6707	Sequence 6707, Ap	229	37.5	42.1	13	2	US-10-158-825-118	Sequence 118, App
157	39	43.8	419	2	US-09-252-991A-28413	Sequence 28413, A	230	37.5	42.1	94	2	US-09-688-017-321	Sequence 321, App
158	39	43.8	427	2	US-08-311-731A-68	Sequence 68, Appl	231	37.5	42.1	934	2	US-09-949-002-289	Sequence 289, App
159	39	43.8	474	2	US-08-311-731A-318	Sequence 318, App	232	37.5	42.1	981	2	US-09-949-002-513	Sequence 513, App
160	39	43.8	493	2	US-09-543-681A-4617	Sequence 4617, Ap	233	37	41.6	33	2	US-08-624-735B-15	Sequence 15, Appl
161	39	43.8	504	2	US-09-252-991A-28242	Sequence 28242, A	234	37	41.6	33	2	US-08-624-735B-16	Sequence 16, Appl
162	39	43.8	993	1	US-08-183-211-2	Sequence 2, Appll	235	37	41.6	35	2	US-09-270-767-61676	Sequence 61676, A
163	39	43.8	993	4	PCT-US95-00176A-2	Sequence 2, Appll	236	37	41.6	60	2	US-09-248-796A-23302	Sequence 23302, A
164	39	43.8	1024	2	US-09-562-737-83	Sequence 83, Appl	237	37	41.6	85	2	US-09-599-632-23	Sequence 23, Appl
165	38.5	43.3	80	2	US-08-624-735E-8	Sequence 8, Appll	238	37	41.6	85	2	US-09-540-236-2635	Sequence 2635, Ap
166	38.5	43.3	488	2	US-09-538-092-1367	Sequence 1367, Ap	239	37	41.6	118	2	US-09-252-991A-20313	Sequence 20313, A
167	38.5	43.3	488	2	US-10-239-333B-6	Sequence 6, Appll	240	37	41.6	118	2	US-09-252-991A-21190	Sequence 21190, A
168	38.5	43.3	556	2	US-09-949-016-7424	Sequence 7424, Ap	241	37	41.6	121	2	US-09-252-991A-29945	Sequence 29945, A
169	38	42.7	20	2	US-09-962-756-996	Sequence 996, App	242	37	41.6	125	2	US-08-624-725E-7	Sequence 7, Appll
170	38	42.7	48	2	US-08-630-916A-72	Sequence 72, Appl	243	37	41.6	134	2	US-09-270-767-46122	Sequence 46122, A
171	38	42.7	118	2	US-09-513-999C-8155	Sequence 8155, Ap	244	37	41.6	168	2	US-09-053-197A-20	Sequence 20, Appl
172	38	42.7	146	2	US-09-252-991A-17306	Sequence 17306, A	245	37	41.6	168	2	US-09-085-761A-20	Sequence 20, Appl
173	38	42.7	147	2	US-09-248-796A-19986	Sequence 19986, A	246	37	41.6	179	2	US-09-252-991A-24507	Sequence 24507, A

247	37	41.6	180	2	US-09-252-991A-18269	Sequence 18269, A	320	36.5	41.0	57	4	PCT-US93-08528-251	Sequence 251, App
248	37	41.6	217	2	US-09-746-359A-38	Sequence 38, App	321	36.5	41.0	60	1	US-08-118-270-252	Sequence 252, App
249	37	41.6	251	2	US-10-104-047-3110	Sequence 3110, App	322	36.5	41.0	60	1	US-08-118-270-253	Sequence 253, App
250	37	41.6	281	2	US-09-248-796A-18801	Sequence 18801, A	323	36.5	41.0	60	4	PCT-US93-08528-252	Sequence 252, App
251	37	41.6	281	2	US-09-252-991A-23962	Sequence 23962, A	324	36.5	41.0	60	4	PCT-US93-08528-253	Sequence 253, App
252	37	41.6	320	2	US-09-248-796A-15998	Sequence 15998, A	325	36.5	41.0	134	2	US-09-252-991A-18017	Sequence 18017, A
253	37	41.6	323	2	US-09-702-705-1821	Sequence 1821, A	326	36.5	41.0	321	1	US-08-118-270-23	Sequence 23, Appl
254	37	41.6	323	2	US-09-736-457-1821	Sequence 1821, App	327	36.5	41.0	321	4	PCT-US93-08528-23	Sequence 23, Appl
255	37	41.6	323	2	US-09-671-325-1821	Sequence 1821, App	328	36.5	41.0	576	2	PCT-US93-08528-23	Sequence 23, Appl
256	37	41.6	323	2	US-10-017-754-1821	Sequence 1821, App	329	36.5	41.0	601	1	US-07-676-174A-2	Sequence 2, Appl
257	37	41.6	344	2	US-09-252-991A-22486	Sequence 22486, A	330	36.5	41.0	601	1	US-08-194-338-2	Sequence 2, Appl
258	37	41.6	344	2	US-09-370-767-44158	Sequence 44158, A	331	36.5	41.0	979	1	US-08-308-881-6	Sequence 6, Appl
259	37	41.6	346	2	US-09-252-991A-31107	Sequence 31107, A	332	36.5	41.0	979	1	US-09-058-263-6	Sequence 6, Appl
260	37	41.6	364	2	US-08-643-597-172	Sequence 172, App	333	36.5	41.0	979	1	US-09-059-099-6	Sequence 6, Appl
261	37	41.6	364	2	US-09-480-884A-172	Sequence 172, App	334	36.5	41.0	979	2	US-09-058-264-6	Sequence 6, Appl
262	37	41.6	364	2	US-09-702-705-783	Sequence 783, App	335	36.5	41.0	979	2	US-09-455-962-6	Sequence 6, Appl
263	37	41.6	364	2	US-09-736-457-783	Sequence 783, App	336	36.5	41.0	979	2	PCT-US95-06530-6	Sequence 6, Appl
264	37	41.6	364	2	US-09-542-615A-172	Sequence 172, App	337	36.5	41.0	1207	2	US-09-817-762-7	Sequence 7, Appl
265	37	41.6	364	2	US-09-606-421B-172	Sequence 172, App	338	36	40.4	8	1	US-08-397-101-16	Sequence 16, Appl
266	37	41.6	364	2	US-09-614-1248-783	Sequence 783, App	339	36	40.4	8	4	PCT-US93-08436-16	Sequence 16, Appl
267	37	41.6	364	2	US-09-671-325-783	Sequence 783, App	340	36	40.4	9	1	US-08-397-101-9	Sequence 9, Appl
268	37	41.6	364	2	US-09-589-184-783	Sequence 783, App	341	36	40.4	9	1	US-08-397-101-10	Sequence 10, Appl
269	37	41.6	364	2	US-09-466-396A-172	Sequence 172, App	342	36	40.4	9	4	PCT-US93-08436-9	Sequence 9, Appl
270	37	41.6	364	2	US-09-476-496A-172	Sequence 172, App	343	36	40.4	9	4	PCT-US93-08436-8	Sequence 8, Appl
271	37	41.6	364	2	US-09-630-940B-172	Sequence 172, App	344	36	40.4	9	4	PCT-US93-08436-15	Sequence 15, Appl
272	37	41.6	364	2	US-09-658-824-783	Sequence 783, App	345	36	40.4	10	1	US-08-397-101-8	Sequence 8, Appl
273	37	41.6	364	2	US-09-285-479-172	Sequence 172, App	346	36	40.4	10	1	US-08-397-101-11	Sequence 11, Appl
274	37	41.6	364	2	US-10-017-754-783	Sequence 783, App	347	36	40.4	10	1	US-08-397-101-13	Sequence 13, Appl
275	37	41.6	364	2	US-09-651-563-783	Sequence 783, App	348	36	40.4	10	1	US-08-397-101-19	Sequence 19, Appl
276	37	41.6	364	2	US-09-619-642-783	Sequence 783, App	349	36	40.4	10	4	PCT-US93-08436-11	Sequence 11, Appl
277	37	41.6	364	2	US-10-007-700-172	Sequence 172, App	350	36	40.4	10	4	PCT-US93-08436-13	Sequence 13, Appl
278	37	41.6	371	2	US-10-007-700-433	Sequence 433, App	351	36	40.4	10	4	PCT-US93-08436-15	Sequence 15, Appl
279	37	41.6	376	2	US-09-202-767-43474	Sequence 43474, A	352	36	40.4	10	4	PCT-US93-08436-19	Sequence 19, Appl
280	37	41.6	412	2	US-09-502-540-15974	Sequence 15974, A	353	36	40.4	12	2	US-09-836-770A-3	Sequence 3, Appl
281	37	41.6	428	2	US-09-538-092-828	Sequence 828, App	354	36	40.4	12	2	US-10-158-847-110	Sequence 110, App
282	37	41.6	431	2	US-09-239-333B-7	Sequence 7, Appl	355	36	40.4	13	2	US-10-158-847-111	Sequence 111, App
283	37	41.6	465	2	US-09-949-016-10173	Sequence 10173, A	356	36	40.4	13	2	US-10-158-825-111	Sequence 111, App
284	37	41.6	480	2	US-09-349-016-10909	Sequence 10909, A	357	36	40.4	13	2	US-10-158-825-111	Sequence 111, App
285	37	41.6	481	2	US-10-239-333B-5	Sequence 5, Appl	358	36	40.4	20	1	US-09-067-379-8	Sequence 8, Appl
286	37	41.6	481	2	US-09-538-092-1308	Sequence 1308, App	359	36	40.4	20	2	US-09-471-276-976	Sequence 976, App
287	37	41.6	482	2	US-09-624-735B-5	Sequence 5, Appl	360	36	40.4	60	1	US-08-451-472-6	Sequence 25, Appl
288	37	41.6	504	2	US-09-252-991A-19852	Sequence 19852, A	361	36	40.4	61	1	US-08-682-485A-25	Sequence 25, Appl
289	37	41.6	510	2	US-09-349-016-10933	Sequence 10933, A	362	36	40.4	61	1	US-08-682-485A-26	Sequence 26, Appl
290	37	41.6	513	2	US-10-012-331A-385	Sequence 385, App	363	36	40.4	61	1	US-08-451-472-4	Sequence 4, Appl
291	37	41.6	513	2	US-10-015-389A-385	Sequence 385, App	364	36	40.4	61	1	US-08-933-314-25	Sequence 25, Appl
292	37	41.6	513	2	US-10-006-768A-385	Sequence 385, App	365	36	40.4	61	1	US-08-472-053-2	Sequence 2, Appl
293	37	41.6	513	2	US-10-015-671A-385	Sequence 385, App	366	36	40.4	61	2	US-08-472-053-3	Sequence 3, Appl
294	37	41.6	513	2	US-10-015-393A-385	Sequence 385, App	367	36	40.4	61	2	US-08-472-053-4	Sequence 4, Appl
295	37	41.6	513	2	US-10-015-393A-385	Sequence 385, App	368	36	40.4	62	1	US-08-472-053-5	Sequence 5, Appl
296	37	41.6	513	2	US-10-006-041A-385	Sequence 385, App	369	36	40.4	62	2	US-08-472-053-6	Sequence 6, Appl
297	37	41.6	513	2	US-09-746-359A-39	Sequence 39, App	370	36	40.4	78	1	US-08-465-380-53	Sequence 53, Appl
298	37	41.6	514	2	US-09-746-359A-39	Sequence 39, App	371	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
299	37	41.6	546	2	US-09-252-991A-22418	Sequence 22418, A	372	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
300	37	41.6	618	2	US-09-328-352-6021	Sequence 6021, App	373	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
301	37	41.6	659	2	US-09-457-040B-18	Sequence 18, App	374	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
302	37	41.6	699	2	US-09-457-040B-18	Sequence 18, App	375	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
303	37	41.6	712	2	US-09-902-540-10691	Sequence 10691, A	376	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
304	37	41.6	732	2	US-09-949-016-9783	Sequence 9783, App	377	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
305	37	41.6	966	1	US-08-571-758-2	Sequence 2, Appl	378	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
306	37	41.6	966	1	US-08-909-984A-2	Sequence 2, Appl	379	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
307	37	41.6	966	1	US-08-909-984A-2	Sequence 2, Appl	380	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
308	37	41.6	1003	1	US-08-909-984A-4	Sequence 4, Appl	381	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
309	37	41.6	1003	1	US-08-909-984A-4	Sequence 4, Appl	382	36	40.4	78	1	US-08-465-380-54	Sequence 54, Appl
310	37	41.6	1003	1	US-08-909-984A-4	Sequence 4, Appl	383	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
311	37	41.6	1133	2	US-09-902-540-12243	Sequence 12243, A	384	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
312	37	41.6	1133	2	US-09-962-756-939	Sequence 939, App	385	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
313	36.5	41.0	36	1	US-08-118-270-231	Sequence 231, App	386	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
314	36.5	41.0	36	1	PCT-US93-08528-231	Sequence 231, App	387	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
315	36.5	41.0	36	4	US-09-513-999C-7368	Sequence 7368, App	388	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
316	36.5	41.0	52	2	US-08-118-270-250	Sequence 250, App	389	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
317	36.5	41.0	56	1	PCT-US93-08528-250	Sequence 250, App	390	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
318	36.5	41.0	56	1	US-08-118-270-251	Sequence 251, App	391	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl
319	36.5	41.0	57	1	US-08-118-270-251	Sequence 251, App	392	36	40.4	78	2	US-09-249-471-53	Sequence 53, Appl

393	36	40.4	78	2	US-09-249-448-53	Sequence 53, Appl	466	36	40.4	382	2	US-09-902-775A-137	Sequence 137, App
394	36	40.4	78	2	US-09-249-448-54	Sequence 54, Appl	467	36	40.4	382	2	US-09-906-700-137	Sequence 137, App
395	36	40.4	78	2	US-09-249-473-53	Sequence 53, Appl	468	36	40.4	382	2	US-09-903-603A-137	Sequence 137, App
396	36	40.4	78	2	US-09-249-473-54	Sequence 54, Appl	469	36	40.4	382	2	US-09-904-920A-137	Sequence 137, App
397	36	40.4	78	2	US-09-498-556-53	Sequence 53, Appl	470	36	40.4	382	2	US-09-909-064-137	Sequence 137, App
398	36	40.4	78	2	US-09-498-556-54	Sequence 54, Appl	471	36	40.4	382	2	US-09-905-381A-137	Sequence 137, App
399	36	40.4	80	2	US-09-952-333A-14	Sequence 14, Appl	472	36	40.4	382	2	US-09-906-618-137	Sequence 137, App
400	36	40.4	80	2	US-08-970-264A-27	Sequence 27, Appl	473	36	40.4	382	2	US-09-906-646-137	Sequence 137, App
401	36	40.4	85	2	US-09-599-632-22	Sequence 22, Appl	474	36	40.4	382	2	US-09-904-462-137	Sequence 137, App
402	36	40.4	87	2	US-09-991-181-175	Sequence 175, App	475	36	40.4	382	2	US-09-902-736A-137	Sequence 137, App
403	36	40.4	87	2	US-09-990-444-175	Sequence 175, App	476	36	40.4	382	2	US-09-906-722A-137	Sequence 137, App
404	36	40.4	87	2	US-09-997-333-175	Sequence 175, App	477	36	40.4	382	2	US-09-198-452A-933	Sequence 933, App
405	36	40.4	87	2	US-09-992-538-175	Sequence 175, App	478	36	40.4	401	2	US-09-252-991A-32529	Sequence 32529, A
406	36	40.4	93	2	US-09-252-991A-17144	Sequence 17144, A	479	36	40.4	415	2	US-09-809-665A-69	Sequence 69, Appl
407	36	40.4	102	2	US-09-621-976-6356	Sequence 6356, Ap	480	36	40.4	426	1	US-08-631-607-6	Sequence 6, Appl
408	36	40.4	115	2	US-09-252-991A-28403	Sequence 28403, A	481	36	40.4	426	1	US-09-998-358B-6	Sequence 6, Appl
409	36	40.4	116	2	US-08-838-682-13	Sequence 13, Appl	482	36	40.4	430	1	US-08-631-607-7	Sequence 7, Appl
410	36	40.4	116	2	US-08-895-914-13	Sequence 13, Appl	483	36	40.4	430	1	US-09-998-358B-7	Sequence 7, Appl
411	36	40.4	116	2	US-09-357-710A-13	Sequence 13, Appl	484	36	40.4	430	2	US-09-949-016-6234	Sequence 2, Appl
412	36	40.4	116	2	US-09-357-707-13	Sequence 13, Appl	485	36	40.4	432	1	US-08-631-607-2	Sequence 2, Appl
413	36	40.4	116	2	US-09-357-708-13	Sequence 13, Appl	486	36	40.4	432	2	US-09-998-358B-2	Sequence 2, Appl
414	36	40.4	116	2	US-09-605-703B-850	Sequence 850, App	487	36	40.4	455	2	US-09-270-767-33247	Sequence 33247, A
415	36	40.4	135	2	US-09-252-991A-19618	Sequence 19618, A	488	36	40.4	455	2	US-09-270-767-48464	Sequence 48464, A
416	36	40.4	140	2	US-09-540-236-2770	Sequence 2770, Ap	489	36	40.4	472	2	US-09-328-352-6870	Sequence 6870, Ap
417	36	40.4	154	2	US-09-710-279-712	Sequence 712, App	490	36	40.4	479	1	US-08-942-218A-2	Sequence 2, Appl
418	36	40.4	155	2	US-09-134-001C-3017	Sequence 3017, Ap	491	36	40.4	492	2	US-09-270-767-32213	Sequence 32213, A
419	36	40.4	159	2	US-10-104-047-2779	Sequence 2779, Ap	492	36	40.4	492	2	US-09-270-767-47430	Sequence 47430, A
420	36	40.4	162	1	US-08-465-380-63	Sequence 63, Appl	493	36	40.4	499	1	US-08-610-731A-2	Sequence 2, Appl
421	36	40.4	162	1	US-08-465-380-64	Sequence 64, Appl	494	36	40.4	499	1	US-09-067-379-2	Sequence 2, Appl
422	36	40.4	162	1	US-08-486-397-63	Sequence 63, Appl	495	36	40.4	499	2	US-09-067-506-2	Sequence 2, Appl
423	36	40.4	162	1	US-08-486-397-64	Sequence 64, Appl	496	36	40.4	499	2	US-08-951-034B-2	Sequence 2, Appl
424	36	40.4	162	1	US-08-486-399-63	Sequence 63, Appl	497	36	40.4	609	2	US-09-270-767-46418	Sequence 46418, A
425	36	40.4	162	1	US-08-486-399-64	Sequence 64, Appl	498	36	40.4	610	2	US-08-368-776A-3	Sequence 3, Appl
426	36	40.4	162	1	US-08-461-965-63	Sequence 63, Appl	499	36	40.4	626	4	PCT-US96-00419-3	Sequence 3, Appl
427	36	40.4	162	1	US-08-461-965-64	Sequence 64, Appl	500	36	40.4	626	4	US-08-368-776A-5	Sequence 5, Appl
428	36	40.4	162	1	US-08-634-641-63	Sequence 63, Appl	501	36	40.4	626	4	PCT-US96-00419-5	Sequence 5, Appl
429	36	40.4	162	1	US-08-634-641-64	Sequence 64, Appl	502	36	40.4	646	2	US-09-248-796A-20617	Sequence 20617, A
430	36	40.4	162	2	US-09-249-471-63	Sequence 63, Appl	503	36	40.4	722	2	US-09-942-711-16	Sequence 16, Appl
431	36	40.4	162	2	US-09-249-471-64	Sequence 64, Appl	504	36	40.4	726	2	US-09-126-980-2	Sequence 2, Appl
432	36	40.4	162	2	US-09-249-472-63	Sequence 63, Appl	505	36	40.4	726	2	US-09-476-482-2	Sequence 2, Appl
433	36	40.4	162	2	US-09-249-472-64	Sequence 64, Appl	506	36	40.4	726	2	US-09-517-605-6	Sequence 6, Appl
434	36	40.4	162	2	US-09-249-472-65	Sequence 65, Appl	507	36	40.4	726	2	US-09-569-611C-43	Sequence 43, Appl
435	36	40.4	162	2	US-09-249-472-66	Sequence 66, Appl	508	36	40.4	785	2	US-08-306-546C-2	Sequence 2, Appl
436	36	40.4	162	2	US-08-809-455-63	Sequence 63, Appl	509	36	40.4	879	1	US-08-530-524A-2	Sequence 2, Appl
437	36	40.4	162	2	US-08-809-455-64	Sequence 64, Appl	510	36	40.4	879	1	US-09-942-711-19	Sequence 19, Appl
438	36	40.4	162	2	US-09-249-461-63	Sequence 63, Appl	511	36	40.4	983	2	US-09-942-711-18	Sequence 18, Appl
439	36	40.4	162	2	US-09-249-461-64	Sequence 64, Appl	512	36	40.4	984	2	US-09-287-354-2	Sequence 2, Appl
440	36	40.4	162	2	US-09-249-461-65	Sequence 65, Appl	513	36	40.4	986	2	US-09-942-711-20	Sequence 20, Appl
441	36	40.4	162	2	US-09-249-461-66	Sequence 66, Appl	514	36	40.4	986	2	US-07-813-593-2	Sequence 2, Appl
442	36	40.4	162	2	US-09-249-473-63	Sequence 63, Appl	515	36	40.4	992	1	US-07-977-451-2	Sequence 2, Appl
443	36	40.4	162	2	US-09-249-473-64	Sequence 64, Appl	516	36	40.4	992	1	US-07-946-507-2	Sequence 2, Appl
444	36	40.4	162	2	US-09-498-556-63	Sequence 63, Appl	517	36	40.4	992	1	US-08-252-517-2	Sequence 2, Appl
445	36	40.4	162	2	US-09-498-556-64	Sequence 64, Appl	518	36	40.4	992	1	US-07-906-397A-2	Sequence 2, Appl
446	36	40.4	180	2	US-09-270-767-48862	Sequence 48862, A	519	36	40.4	992	1	US-07-906-397A-2	Sequence 2, Appl
447	36	40.4	189	2	US-09-252-991A-32376	Sequence 32376, A	520	36	40.4	992	1	US-08-601-891-2	Sequence 2, Appl
448	36	40.4	200	2	US-09-902-540-16501	Sequence 16501, A	521	36	40.4	992	1	US-09-021-324-2	Sequence 2, Appl
449	36	40.4	209	2	US-09-345-473E-6	Sequence 6, Appl	522	36	40.4	992	2	US-09-872-136B-2	Sequence 2, Appl
450	36	40.4	209	2	US-09-862-027-6	Sequence 6, Appl	523	36	40.4	992	2	US-09-919-408A-2	Sequence 2, Appl
451	36	40.4	217	2	US-09-949-016-11621	Sequence 11621, A	524	36	40.4	992	4	PCT-US92-02750-2	Sequence 2, Appl
452	36	40.4	232	1	US-08-631-607-5	Sequence 5, Appl	525	36	40.4	992	4	PCT-US92-05401-2	Sequence 2, Appl
453	36	40.4	232	2	US-09-098-358B-5	Sequence 5, Appl	526	36	40.4	992	4	PCT-US92-09893-2	Sequence 2, Appl
454	36	40.4	232	2	US-09-134-000C-6750	Sequence 6750, Ap	527	36	40.4	993	1	US-07-977-451-4	Sequence 4, Appl
455	36	40.4	232	2	US-07-857-224B-61	Sequence 61, Appl	528	36	40.4	993	1	US-08-252-517-4	Sequence 4, Appl
456	36	40.4	261	1	US-09-252-991A-24262	Sequence 24262, A	529	36	40.4	993	1	US-07-906-397A-4	Sequence 4, Appl
457	36	40.4	264	2	US-09-252-991A-28205	Sequence 28205, A	530	36	40.4	993	1	US-08-222-299-4	Sequence 4, Appl
458	36	40.4	302	2	US-08-853-839-2	Sequence 2, Appl	531	36	40.4	993	1	US-08-601-891-4	Sequence 4, Appl
459	36	40.4	323	2	US-09-498-039A-8632	Sequence 8632, Ap	532	36	40.4	993	1	US-09-021-324-4	Sequence 4, Appl
460	36	40.4	348	2	US-09-252-991A-26426	Sequence 26426, A	533	36	40.4	993	1	US-08-434-878-4	Sequence 4, Appl
461	36	40.4	364	2	US-09-489-847-166	Sequence 166, App	534	36	40.4	993	2	US-08-368-776A-11	Sequence 11, Appl
462	36	40.4	374	2	US-09-253-991A-28320	Sequence 28320, A	535	36	40.4	993	2	US-09-872-136B-4	Sequence 4, Appl
463	36	40.4	381	2	US-09-907-794A-137	Sequence 137, App	536	36	40.4	993	2	US-09-919-408A-4	Sequence 4, Appl
464	36	40.4	382	2	US-09-905-125A-137	Sequence 137, App	537	36	40.4	993	4	PCT-US92-09893-4	Sequence 4, Appl
465	36	40.4	382	2			538	36	40.4	993	4	PCT-US95-03718-4	Sequence 4, Appl

539	36	40.4	994	2	US-08-368-776A-12	Sequence 12, Appl	612	35	39.3	103	2	US-10-004-860-587	Sequence 587, App
540	36	40.4	994	2	US-09-942-711-17	Sequence 17, Appl	613	35	39.3	107	2	US-09-248-796A-27787	Sequence 27787, A
541	36	40.4	998	1	US-08-449-645A-17	Sequence 17, Appl	614	35	39.3	112	2	US-09-252-991A-26083	Sequence 26083, A
542	36	40.4	998	1	US-08-702-367A-17	Sequence 17, Appl	615	35	39.3	129	2	US-10-104-047-2426	Sequence 2426, App
543	36	40.4	998	2	US-08-368-776A-2	Sequence 2, Appl	616	35	39.3	133	2	US-09-732-210-1661	Sequence 1661, App
544	36	40.4	998	2	US-09-949-016-6501	Sequence 6501, App	617	35	39.3	141	2	US-09-270-767-48991	Sequence 48991, A
545	36	40.4	998	4	PCT-US95-04681-17	Sequence 17, Appl	618	35	39.3	142	2	US-09-380-882-9	Sequence 9, Appl
546	36	40.4	998	4	PCT-US96-00419-2	Sequence 2, Appl	619	35	39.3	153	2	US-09-270-767-36877	Sequence 36877, A
547	36	40.4	1000	1	US-08-222-299-2	Sequence 2, Appl	620	35	39.3	153	2	US-09-270-767-52094	Sequence 52094, A
548	36	40.4	1000	1	US-08-434-878-2	Sequence 2, Appl	621	35	39.3	154	2	US-09-252-991A-25483	Sequence 25483, A
549	36	40.4	1000	4	PCT-US95-03718-2	Sequence 2, Appl	622	35	39.3	154	2	US-09-248-796A-24748	Sequence 24748, A
550	36	40.4	1005	2	US-09-949-016-9901	Sequence 9901, App	623	35	39.3	160	2	US-09-252-991A-22085	Sequence 22085, A
551	36	40.4	1044	4	US-10-101-464A-956	Sequence 956, App	624	35	39.3	177	2	US-09-252-991A-31950	Sequence 31950, A
552	36	40.4	1160	4	PCT-US92-05401-4	Sequence 4, Appl	625	35	39.3	179	2	US-09-328-352-4469	Sequence 4469, App
553	36	40.4	1182	2	US-09-287-354-6	Sequence 6, Appl	626	35	39.3	180	2	US-09-252-991A-32278	Sequence 32278, A
554	36	40.4	1189	2	US-09-287-354-3	Sequence 3, Appl	627	35	39.3	197	2	US-08-974-022-49	Sequence 49, Appl
555	36	40.4	1189	2	US-09-287-354-4	Sequence 4, Appl	628	35	39.3	197	2	US-08-795-445A-49	Sequence 49, Appl
556	36	40.4	1189	2	US-09-949-016-6931	Sequence 6931, App	629	35	39.3	197	2	US-08-795-447A-49	Sequence 49, Appl
557	36	40.4	1207	2	US-09-287-354-5	Sequence 5, Appl	630	35	39.3	197	2	US-08-974-186-49	Sequence 49, Appl
558	36	40.4	1754	1	US-07-745-206A-13	Sequence 13, Appl	631	35	39.3	197	2	US-08-795-446B-49	Sequence 49, Appl
559	36	40.4	1754	1	US-08-311-363-13	Sequence 13, Appl	632	35	39.3	197	2	US-08-706-945D-135	Sequence 135, App
560	36	40.4	2594	2	US-08-718-388-7	Sequence 7, Appl	633	35	39.3	197	2	US-08-577-788C-49	Sequence 49, Appl
561	36	40.4	3025	6	5223423-3	Patent No. 5223423	634	35	39.3	222	2	US-09-328-352-6281	Sequence 6281, App
562	36	40.4	5405	2	US-08-718-388-9	Sequence 9, Appl	635	35	39.3	249	2	US-09-328-352-6476	Sequence 6476, App
563	35.5	39.9	79	2	US-09-513-999C-7087	Sequence 7087, App	636	35	39.3	255	2	US-09-252-991A-22733	Sequence 22733, A
564	35.5	39.9	88	2	US-09-270-767-42897	Sequence 42897, A	637	35	39.3	257	2	US-09-252-991A-19921	Sequence 19921, A
565	35.5	39.9	180	2	US-09-252-991A-28489	Sequence 28489, A	638	35	39.3	261	1	US-07-857-224B-59	Sequence 59, Appl
566	35.5	39.9	186	2	US-09-252-991A-20433	Sequence 20433, A	639	35	39.3	275	1	US-08-701-191A-36	Sequence 36, Appl
567	35.5	39.9	191	2	US-09-252-991A-18732	Sequence 18732, A	640	35	39.3	275	1	US-09-664-526-36	Sequence 36, Appl
568	35.5	39.9	232	1	US-08-685-992-27	Sequence 27, Appl	641	35	39.3	289	2	US-09-042-785A-11	Sequence 11, Appl
569	35.5	39.9	232	1	US-09-144-925-27	Sequence 27, Appl	642	35	39.3	313	2	US-09-270-767-35391	Sequence 35391, A
570	35.5	39.9	233	1	US-08-015-985-11	Sequence 11, Appl	643	35	39.3	313	2	US-09-270-767-50608	Sequence 50608, A
571	35.5	39.9	233	1	US-09-280-597-11	Sequence 11, Appl	644	35	39.3	318	1	US-08-701-191A-10	Sequence 10, Appl
572	35.5	39.9	232	2	US-09-949-016-6472	Sequence 16, Appl	645	35	39.3	318	2	US-09-664-526-10	Sequence 10, Appl
573	35.5	39.9	253	2	US-09-949-016-9375	Sequence 3755, App	646	35	39.3	326	2	US-09-949-016-6679	Sequence 6679, App
574	35.5	39.9	236	2	US-09-252-991A-32162	Sequence 32162, A	647	35	39.3	341	2	US-09-902-540-11473	Sequence 11473, A
575	35.5	39.9	351	1	US-08-415-751-41	Sequence 41, Appl	648	35	39.3	342	2	US-09-252-991A-23584	Sequence 23584, A
576	35.5	39.9	373	2	US-09-252-991A-24545	Sequence 24545, A	649	35	39.3	343	2	US-09-252-991A-22307	Sequence 22307, A
577	35.5	39.9	454	2	US-10-104-047-2092	Sequence 2092, App	650	35	39.3	346	2	US-09-073-297-2	Sequence 2, Appl
578	35.5	39.9	793	1	US-08-015-985-3	Sequence 3, Appl	651	35	39.3	347	2	US-09-949-016-11456	Sequence 11456, A
579	35.5	39.9	793	1	US-09-280-597-3	Sequence 3, Appl	652	35	39.3	350	2	US-09-252-991A-29860	Sequence 29860, A
580	35.5	39.9	802	1	US-08-015-985-1	Sequence 1, Appl	653	35	39.3	366	2	US-08-857-076-103	Sequence 103, App
581	35.5	39.9	802	1	US-09-280-597-1	Sequence 1, Appl	654	35	39.3	366	2	US-09-205-658-103	Sequence 103, App
582	35.5	39.9	807	2	US-09-949-016-7356	Sequence 7356, App	655	35	39.3	368	2	US-09-538-092-300	Sequence 32075, A
583	35	39.3	12	2	US-09-836-770A-1	Sequence 1, Appl	656	35	39.3	380	2	US-09-538-092-300	Sequence 300, App
584	35	39.3	13	2	US-10-158-847-106	Sequence 106, App	657	35	39.3	382	2	US-09-252-991A-25554	Sequence 25554, A
585	35	39.3	13	2	US-10-158-847-108	Sequence 108, App	658	35	39.3	384	1	US-08-673-388-11	Sequence 11, Appl
586	35	39.3	13	2	US-10-158-825-106	Sequence 106, App	659	35	39.3	384	1	US-08-614-877-11	Sequence 11, Appl
587	35	39.3	13	2	US-10-158-825-108	Sequence 108, App	660	35	39.3	385	2	US-09-252-991A-25651	Sequence 25651, A
588	35	39.3	14	2	US-10-158-847-115	Sequence 115, App	661	35	39.3	419	2	US-09-198-452A-974	Sequence 974, App
589	35	39.3	14	2	US-10-158-825-115	Sequence 115, App	662	35	39.3	422	1	US-08-190-802A-52	Sequence 52, Appl
590	35	39.3	20	2	US-09-362-756-960	Sequence 960, App	663	35	39.3	422	2	US-08-477-346-52	Sequence 52, Appl
591	35	39.3	29	1	US-08-637-759B-304	Sequence 304, App	664	35	39.3	422	2	US-08-473-089-52	Sequence 52, Appl
592	35	39.3	29	2	US-08-871-355A-304	Sequence 304, App	665	35	39.3	422	2	US-08-487-072A-52	Sequence 52, Appl
593	35	39.3	29	2	US-09-201-945-304	Sequence 304, App	666	35	39.3	422	2	US-09-385-219A-4	Sequence 4, Appl
594	35	39.3	42	2	US-09-177-249-213	Sequence 213, App	667	35	39.3	423	2	US-09-181-339-9	Sequence 9, Appl
595	35	39.3	42	2	US-09-812-283-213	Sequence 213, App	668	35	39.3	432	2	US-09-583-110-4915	Sequence 4915, App
596	35	39.3	58	2	US-09-270-767-38193	Sequence 38193, A	669	35	39.3	433	2	US-09-438-185A-903	Sequence 903, App
597	35	39.3	58	2	US-09-270-767-53410	Sequence 53410, A	670	35	39.3	440	1	US-08-307-499-15	Sequence 15, Appl
598	35	39.3	62	2	US-09-270-767-37803	Sequence 37803, A	671	35	39.3	440	1	US-09-299-268-15	Sequence 15, Appl
599	35	39.3	62	2	US-09-270-767-53020	Sequence 53020, A	672	35	39.3	443	2	US-09-328-352-7207	Sequence 7207, App
600	35	39.3	64	2	US-09-205-258-1109	Sequence 1109, App	673	35	39.3	443	2	US-09-107-433-2783	Sequence 2783, App
601	35	39.3	64	2	US-10-004-860-1109	Sequence 1109, App	674	35	39.3	469	2	US-09-252-991A-25581	Sequence 25581, A
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603	35	39.3	75	2	US-09-973-278-203	Sequence 203, App	676	35	39.3	486	2	US-08-746-559A-5	Sequence 5, Appl
604	35	39.3	76	2	US-09-227-357-261	Sequence 261, App	677	35	39.3	490	2	US-09-336-643A-6	Sequence 6, Appl
605	35	39.3	76	2	US-09-248-796A-26451	Sequence 26451, A	678	35	39.3	491	2	US-09-181-339-7	Sequence 7, Appl
606	35	39.3	78	2	US-09-073-297-18	Sequence 18, Appl	679	35	39.3	491	2	US-09-181-339-12	Sequence 12, Appl
607	35	39.3	95	2	US-09-270-767-47319	Sequence 47319, A	680	35	39.3	507	2	US-09-949-016-9860	Sequence 9860, App
608	35	39.3	98	2	US-09-461-325-215	Sequence 215, App	681	35	39.3	513	2	US-09-248-796A-20548	Sequence 20548, A
609	35	39.3	98	2	US-10-012-542-215	Sequence 215, App	682	35	39.3	514	2	US-09-266-965-114	Sequence 114, App
610	35	39.3	98	2	US-10-115-123-215	Sequence 215, App	683	35	39.3	516	2	US-08-746-559A-4	Sequence 4, Appl
611	35	39.3	103	2	US-09-205-258-587	Sequence 587, App	684	35	39.3	547	1	US-08-314-615-1	Sequence 1, Appl

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686	35	39.3	547	1	US-08-473-981A-6	Sequence 6, Appli	759	34.5	38.8	1219	2	US-09-566-047-5	Sequence 5, Appli
687	35	39.3	547	1	US-08-433-010-1	Sequence 1, Appli	760	34.5	38.8	1254	2	US-09-949-016-10297	Sequence 10297, A
688	35	39.3	547	1	US-08-482-882-1	Sequence 1, Appli	761	34.5	38.8	5179	2	US-09-538-092-1258	Sequence 1258, Ap
689	35	39.3	547	1	US-08-483-389-1	Sequence 1, Appli	762	34	38.2	12	2	US-09-836-770A-2	Sequence 2, Appli
690	35	39.3	547	1	US-08-487-113D-1	Sequence 1, Appli	763	34	38.2	13	2	US-10-158-847-105	Sequence 105, App
691	35	39.3	547	1	US-08-473-503-1	Sequence 1, Appli	764	34	38.2	13	2	US-10-158-825-105	Sequence 40177, A
692	35	39.3	547	1	US-08-483-932-1	Sequence 1, Appli	765	34	38.2	26	2	US-09-270-767-40177	Sequence 55193, A
693	35	39.3	547	1	US-08-474-087-6	Sequence 6, Appli	766	34	38.2	26	2	US-09-270-767-55393	Sequence 40207, A
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695	35	39.3	547	1	US-08-714-017-1	Sequence 1, Appli	768	34	38.2	30	2	US-09-962-756-2088	Sequence 2088, Ap
696	35	39.3	547	2	US-08-863-790-1	Sequence 1, Appli	769	34	38.2	30	2	US-09-962-756-2089	Sequence 2089, Ap
697	35	39.3	547	2	US-08-475-680-1	Sequence 1, Appli	770	34	38.2	30	2	US-09-674-973A-336	Sequence 336, App
698	35	39.3	547	2	US-08-296-749-1	Sequence 1, Appli	771	34	38.2	46	2	US-08-437-841-2	Sequence 2, Appli
699	35	39.3	547	2	US-08-314-369-1	Sequence 1, Appli	772	34	38.2	51	1	US-08-286-521-2	Sequence 2, Appli
700	35	39.3	679	2	US-09-393-028-2	Sequence 2, Appli	773	34	38.2	51	1	US-08-436-175-2	Sequence 2, Appli
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702	35	39.3	801	2	US-09-252-991A-22729	Sequence 22729, A	775	34	38.2	51	2	US-09-013-896A-7	Sequence 7, Appli
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874	34	38.2	235	2	US-10-017-754-332	Sequence 332, App	947	34	38.2	502	2	US-09-328-857A-4	Sequence 4, Appli
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991 34 38.2 626 4 PCT-US95-00670-2 Sequence 2, Appli
992 34 38.2 630 1 US-08-394-177-5 Sequence 5, Appli
993 34 38.2 630 1 US-08-596-319-2 Sequence 2, Appli
994 34 38.2 630 2 US-08-394-912A-5 Sequence 5, Appli
995 34 38.2 630 2 US-09-333-636-5 Sequence 5, Appli
996 34 38.2 633 1 US-08-250-859-17 Sequence 17, Appli
997 34 38.2 633 1 US-08-490-803-17 Sequence 17, Appli
998 34 38.2 633 1 US-08-457-254-7 Sequence 7, Appli
999 34 38.2 633 4 PCT-US94-08806-17 Sequence 17, Appli
1000 34 38.2 633 4 PCT-US95-01775-17 Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-5389
; Sequence 5389, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5389
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -47..-1
; NAME/KEY: UNSURE
; LOCATION: 5
; OTHER INFORMATION: Xaa = Phe,Leu
US-09-621-976-5389

Query Match 52.8%; Score 47; DB 2; Length 54;
Best Local Similarity 60.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Oy 3 VLCWTWETCE 12
Db 41 VLCWVLSCK 50

RESULT 2
US-09-621-976-5390
; Sequence 5390, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5389
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -47..-1
; NAME/KEY: UNSURE
; LOCATION: 5
; OTHER INFORMATION: Xaa = Phe,Leu
US-09-621-976-5389

Query Match 52.8%; Score 47; DB 2; Length 54;
Best Local Similarity 60.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Oy 3 VLCWTWETCE 12
Db 41 VLCWVLSCK 50

RESULT 3
US-09-252-991A-29811
; Sequence 29811, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29811
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29811

Query Match 51.7%; Score 46; DB 2; Length 407;
Best Local Similarity 46.2%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Oy 1 WEVLCWTWETCER 13
Db 5 WREACWKWKTMVR 17

RESULT 4
US-09-949-016-10235
; Sequence 10235, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 10235
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10235

Query Match          51.1%; Score 45.5; DB 2; Length 126;
Best Local Similarity 46.7%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 WEVLC---WTWTFCE 12
DB 13 WELLCPLMGWQPC 27

RESULT 5
US-09-270-767-40967
; Sequence 40967, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40967
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40967

Query Match          51.1%; Score 45.5; DB 2; Length 169;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 EVLCWTWETCER 13
DB 87 EIFCW-WEKCDK 97

RESULT 6
US-09-270-767-56183
; Sequence 56183, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56183
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56183

Query Match          51.1%; Score 45.5; DB 2; Length 169;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 EVLCWTWETCER 13
DB 87 EIFCW-WEKCDK 97

RESULT 7
US-09-702-705-1818
; Sequence 1818, Application US/09702705
; Patent No. 6504010
```

```
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-1818

Query Match          49.4%; Score 44; DB 2; Length 102;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
DB 55 WRLCWCWWE 63

RESULT 8
US-09-736-457-1818
; Sequence 1818, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1818

Query Match          49.4%; Score 44; DB 2; Length 102;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
DB 55 WRLCWCWWE 63

RESULT 9
US-09-671-325-1818
; Sequence 1818, Application US/09671325
; Patent No. 6667154
```

```

; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-671-325-1818

Query Match 49.4%; Score 44; DB 2; Length 102;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTWE 9
Db 55 WRLWCWWWE 63

RESULT 10
US-10-017-754-1818
; Sequence 1818, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1818
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-017-754-1818

Query Match 49.4%; Score 44; DB 2; Length 102;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTWE 9
Db 55 WRLWCWWWE 63

RESULT 11
US-09-252-991A-23048
; Sequence 23048, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23048
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23048

Query Match 49.4%; Score 44; DB 2; Length 216;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WEVLCWTWET 10
Db 97 WDTSCWYWT 106

RESULT 12
US-09-252-991A-31868
; Sequence 31868, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31868
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-31868

Query Match 49.4%; Score 44; DB 2; Length 257;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CWTWETCER 13
Db 236 CWRWTSR 244

RESULT 13
US-10-158-847-101
; Sequence 101, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 101
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-101

Query Match      48.9%; Score 43.5; DB 2; Length 13;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLCWTWETCE 12
| | | | | | | | | | | | |
Db 1 W-VLCFEWEDCD 11

RESULT 14
US-10-158-825-101
; Sequence 101, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-101

Query Match      48.9%; Score 43.5; DB 2; Length 13;
Best Local Similarity 58.3%; Pred. No. 7.2;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLCWTWETCE 12
| | | | | | | | | | | | |
Db 1 W-VLCFEWEDCD 11

RESULT 15
US-10-158-847-30
; Sequence 30, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-30

Query Match      48.9%; Score 43.5; DB 2; Length 21;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLCWTWETCE 12
| | | | | | | | | | | | |
Db 3 W-VLCFEWEDCD 13
```

```

RESULT 16
US-10-158-825-30
; Sequence 30, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 21
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-30

Query Match      48.9%; Score 43.5; DB 2; Length 21;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 WEVLCWTWETCE 12
| | | | | | | | | | | | |
Db 3 W-VLCFEWEDCD 13

RESULT 17
US-08-851-843A-183
; Sequence 183, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
```

```
;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0029300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 183:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-183

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTW 8
Db 18 WAPLCWAW 25

RESULT 18
US-08-974-549A-302
; Sequence 302, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; APPLICATION DATA:
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 18-APR-1997
; APPLICATION DATA:
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 25-APR-1997
; APPLICATION DATA:
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION DATA:
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 14-AUG-1997
; APPLICATION DATA:
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/912,951
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;
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026100S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-302

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTW 8
Db 18 WAPLCWAW 25

RESULT 19
US-08-854-050-183
; Sequence 183, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; APPLICATION DATA:
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION DATA:
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/946,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
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PRIOR APPLICATION DATA: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-08-854-050-183

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
| | | | |
DB 18 WAPLCWAW 25

RESULT 20

US-09-430-323-183
Sequence 183, Application US/09430323
Patent No. 6309867

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-09-430-323-183

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
| | | | |
DB 18 WAPLCWAW 25

RESULT 21

US-09-402-181B-302
Sequence 302, Application US/09402181B
Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

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; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausehus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 302:
US-09-402-181B-302

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
DB 18 WAPLCWAW 25

RESULT 22
US-09-721-456-302
; Sequence 302, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/911,312

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; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 302:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 302:
US-09-721-456-302

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLCWTW 8
DB 18 WAPLCWAW 25

RESULT 23
US-10-054-295-183
; Sequence 183, Application US/10054295
; Patent No. 6921664
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6921664el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643

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FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 183:
US-10-054-295-183

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTW 8
| | | | |
Db 18 WAPLCWAW 25

RESULT 24
US-09-438-486A-183
Sequence 183, Application US/09438486A
Patent No. 6927285
GENERAL INFORMATION:
APPLICANT: CECH, THOMAS R.
APPLICANT: LINGNER, JOACHIM
APPLICANT: NAKAMURA, TORU
APPLICANT: CHAPMAN, KAREN B.
APPLICANT: MORIN, GREGG B.
APPLICANT: HARLEY, CALVIN
APPLICANT: ANDREWS, WILLIAM H.
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND
TELEOMERASE VARIANTS
FILE REFERENCE: 018/062
CURRENT APPLICATION NUMBER: US/09/438,486A
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 08/851,843
PRIOR FILING DATE: 1997-05-06
PRIOR APPLICATION NUMBER: 08/846,017
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/844,419
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 08/724,643
PRIOR FILING DATE: 1996-10-01
NUMBER OF SEQ ID NOS: 223
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 183
LENGTH: 54
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Recombinant
amino acid sequence
US-09-438-486A-183

Query Match 48.3%; Score 43; DB 2; Length 54;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WEVLCWTW 8
| | | | |
Db 18 WAPLCWAW 25

RESULT 25

US-09-252-991A-30379
Sequence 30379, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30379
LENGTH: 227
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30379
Query Match 48.3%; Score 43; DB 2; Length 227;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CWTWETC 11
| | | | |
Db 62 CWRWTTT 68

RESULT 26
US-09-922-364A-4
Sequence 4, Application US/09922364A
Patent No. 6692937
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Maylie, James
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,364A
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..458
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 1 (rSKI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-922-364A-4
Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 WEVLQWTWETCER 13
DB 212 WIVAATVTRVCER 224
RESULT 27
US-09-254-590-4
; Sequence 4, Application US/09254590
; Patent No. 6797486
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..458
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 1 (rSKI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-254-590-4
Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 WEVLQWTWETCER 13
DB 212 WIVAATVTRVCER 224
RESULT 28
US-10-115-415-4
; Sequence 4, Application US/10115415
; Patent No. 6828122
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,415
FILING DATE: 02-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..458
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 1 (rsk1)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-115-415-4

Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLQWTWETCER 13
DB 212 WIVAATVRCER 224

RESULT 29
US-10-116-260-4
Sequence 4, Application US/10116260
Patent No. 6828123
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,260
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..458
OTHER INFORMATION: /note= "rat small conductance,
calcium-activated potassium channel
protein 1 (rsk1)"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-116-260-4

Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLQWTWETCER 13
DB 212 WIVAATVRCER 224

RESULT 30
US-10-115-671-4
Sequence 4, Application US/10115671
Patent No. 6828420
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,671
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids

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;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..458
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 1 (rSKI)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-115-671-4
Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 212 WIVAATWTVRCER 224

RESULT 31
US-10-115-695-4
; Sequence 4, Application US/10115695
; Patent No. 6894147
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,695
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
;

; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..458
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 1 (rSKI)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-115-695-4
Query Match 48.3%; Score 43; DB 2; Length 458;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 212 WIVAATWTVRCER 224

RESULT 32
US-10-158-847-103
; Sequence 103, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-103
Query Match 47.2%; Score 42; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVLCWTWETC 11
Db 2 IFCFEWETC 10

RESULT 33
US-10-158-825-103
; Sequence 103, Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF555
; CURRENT APPLICATION NUMBER: US/10/158,825
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/294,976
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-825-103
Query Match 47.2%; Score 42; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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US-10-115-415-27
; Sequence 27, Application US/10115415
; Patent No. 6828122
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,415
; FILING DATE: 02-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..328
; OTHER INFORMATION: /note= "core region of hsk1 from
; amino acid positions 124 through 451"
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-115-415-27
Query Match 47.2%; Score 42; DB 2; Length 328;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 WEVLCWTWETCER 13
DB 189 WIIAAWTVRCER 201
RESULT 37
US-10-116-260-27
; Sequence 27, Application US/10116260

; Patent No. 6828123
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/116,260
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..328
; OTHER INFORMATION: /note= "core region of hsk1 from
; amino acid positions 124 through 451"
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-116-260-27
Query Match 47.2%; Score 42; DB 2; Length 328;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 WEVLCWTWETCER 13
DB 189 WIIAAWTVRCER 201
RESULT 38
US-10-115-671-27
; Sequence 27, Application US/10115671
; Patent No. 6828420
; GENERAL INFORMATION:

APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,671
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..328
OTHER INFORMATION: /note= "core region of hsk1 from
amino acid positions 124 through 451"
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-115-671-27
Query Match 47.2%; Score 42; DB 2; Length 328;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WEVLCTWTETCER 13
Db 189 WIIAAWTVRCER 201
RESULT 39
US-10-115-695-27
Sequence 27, Application US/10115695
Patent No. 6894147
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James

Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,695
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..328
OTHER INFORMATION: /note= "core region of hsk1 from
amino acid positions 124 through 451"
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-115-695-27
Query Match 47.2%; Score 42; DB 2; Length 328;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WEVLCTWTETCER 13
Db 189 WIIAAWTVRCER 201
RESULT 40
US-09-949-016-10095
Sequence 10095, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..553
OTHER INFORMATION: /note= "N-terminally truncated form
of rat small conductance,
calcium-activated potassium channel
protein 3 (rsk3)"
FEATURE:
NAME/KEY: Region
LOCATION: 103..436
OTHER INFORMATION: /note= "core region of rsk3"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-922-364A-3

Query Match 47.2%; Score 42; DB 2; Length 386;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| : |||||
Db 129 WIIAAWTVRCER 141

RESULT 41
US-09-922-364A-3
; Sequence 3, Application US/09922364A
; Patent No. 6692937
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,364A
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..553
OTHER INFORMATION: /note= "N-terminally truncated form
of rat small conductance,
calcium-activated potassium channel
protein 3 (rsk3)"
FEATURE:
NAME/KEY: Region
LOCATION: 103..436
OTHER INFORMATION: /note= "core region of rsk3"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-922-364A-3

Query Match 47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| : |||||
Db 297 WIIAAWTVRCER 309

RESULT 42
US-09-254-590-3
; Sequence 3, Application US/09254590
; Patent No. 6797486
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses Thereof

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 553 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..553
;   OTHER INFORMATION: /note= "N-terminally truncated form
;   of rat small conductance,
;   calcium-activated potassium channel
;   protein 3 (rSK3)"
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 109..436
;   OTHER INFORMATION: /note= "core region of rSK3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-254-590-3

Query Match      47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      297 WIITAAWTVRCER 309

RESULT 43
US-10-115-415-3
; Sequence 3, Application US/10115415
; Patent No. 6828122
; GENERAL INFORMATION:
;   APPLICANT: Adelman, John P.
;   Maylie, James
;   Bond, Chris T.
;   Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
;   Calcium-Activated Potassium Channels and Uses
;   Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/115,415
;   FILING DATE: 02-Apr-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/254,590
;   FILING DATE: 10-Mar-1999
;   APPLICATION NUMBER: US 60/026,451
;   FILING DATE: 11-SEP-1996
;   APPLICATION NUMBER: US 60/040,052
;   FILING DATE: 07-MAR-1997
;   APPLICATION NUMBER: US 60/045,233
;   FILING DATE: 17-APR-1997
;   APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Weber, Kenneth A.
;   REGISTRATION NUMBER: 31,677
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; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 553 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
;   NAME/KEY: Protein
;   LOCATION: 1..553
;   OTHER INFORMATION: /note= "N-terminally truncated form
;   of rat small conductance,
;   calcium-activated potassium channel
;   protein 3 (rSK3)"
; FEATURE:
;   NAME/KEY: Region
;   LOCATION: 109..436
;   OTHER INFORMATION: /note= "core region of rSK3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-115-415-3

Query Match      47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      297 WIITAAWTVRCER 309

RESULT 44
US-10-116-260-3
; Sequence 3, Application US/10116260
; Patent No. 6828123
; GENERAL INFORMATION:
;   APPLICANT: Adelman, John P.
;   Maylie, James
;   Bond, Chris T.
;   Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
;   Calcium-Activated Potassium Channels and Uses
;   Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Eighth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94111-3834
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/116,260
;   FILING DATE: 03-Apr-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/254,590
;   FILING DATE: 10-Mar-1999
;   APPLICATION NUMBER: US 60/026,451
;   FILING DATE: 11-SEP-1996
;   APPLICATION NUMBER: US 60/040,052
;   FILING DATE: 07-MAR-1997
;   APPLICATION NUMBER: US 60/045,233
;   FILING DATE: 17-APR-1997
;   APPLICATION NUMBER: WO PCT/US97/16033
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..553
OTHER INFORMATION: /note= "N-terminally truncated form
of rat small conductance,
calcium-activated potassium channel
protein 3 (rSK3)"
FEATURE:
NAME/KEY: Region
LOCATION: 109..436
OTHER INFORMATION: /note= "core region of rSK3"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-116-260-3
Query Match 47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 297 WIIAAWTVRCER 309
RESULT 45
US-10-115-671-3
; Sequence 3, Application US/10115671
; Patent No. 6828420
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels, and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,671
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052

FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..553
OTHER INFORMATION: /note= "N-terminally truncated form
of rat small conductance,
calcium-activated potassium channel
protein 3 (rSK3)"
FEATURE:
NAME/KEY: Region
LOCATION: 109..436
OTHER INFORMATION: /note= "core region of rSK3"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-115-671-3
Query Match 47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 297 WIIAAWTVRCER 309
RESULT 46
US-10-115-695-3
; Sequence 3, Application US/10115695
; Patent No. 6894147
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels, and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/115,695
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590

FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..553
OTHER INFORMATION: /note= "N-terminally truncated form
of rat small conductance,
calcium-activated potassium channel
protein 3 (rSK3)"
FEATURE:
NAME/KEY: Region
LOCATION: 109..436
OTHER INFORMATION: /note= "core region of rSK3"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-115-695-3

Query Match 47.2%; Score 42; DB 2; Length 553;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Db 297 WIIAAWTVRVCER 309

RESULT 47
US-09-922-364A-20
Sequence 20, Application US/09922364A
Patent No. 6692937
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,364A

FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..557
OTHER INFORMATION: /note= "N-terminally truncated form
of human small conductance,
calcium-activated potassium channel
protein 3 (hSK3)"
FEATURE:
NAME/KEY: Region
LOCATION: 109..436
OTHER INFORMATION: /note= "core region of hSK3"
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-922-364A-20

Query Match 47.2%; Score 42; DB 2; Length 557;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
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Db 297 WIIAAWTVRVCER 309

RESULT 48
US-09-254-590-20
Sequence 20, Application US/09254590
Patent No. 6797486
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,260
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-0007300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..557
OTHER INFORMATION: /note= "N-terminally truncated form
of human small conductance,
calcium-activated potassium channel
protein 3 (hSK3)"
FEATURE:
NAME/KEY: Region
LOCATION: 109..436
OTHER INFORMATION: /note= "core region of hSK3"
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-116-260-20
Query Match 47.2%; Score 42; DB 2; Length 557;
Best Local Similarity 46.2%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 WEVLCTWTWCER 13
Db 297 WIIAAWTVRCER 309

Search completed: March 28, 2006, 11:52:28
Job time : 57 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:51:44 ; Search time 166 Seconds
(without alignments)
32.722 Million cell updates/sec

Title: US-10-639-076-4

Perfect score: 89

Sequence: 1 WEVLCTWTCER 13

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Listing first 1000 summaries

Database : Published Applications AA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	89	100.0	15	4	US-10-356-257-4
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7	89	100.0	15	4	US-10-356-257-32
8	89	100.0	16	4	US-10-639-076-17
9	89	100.0	18	4	US-10-639-076-18
10	89	100.0	22	4	US-10-639-076-57
11	89	100.0	24	4	US-10-639-076-19
12	89	100.0	24	4	US-10-639-076-26
13	89	100.0	24	4	US-10-639-076-27
14	89	100.0	24	4	US-10-639-076-39
15	89	100.0	24	4	US-10-639-076-40
16	89	100.0	24	4	US-10-639-076-41
17	88	98.9	15	4	US-10-356-257-17
18	88	98.9	24	4	US-10-639-076-42
19	87	97.8	15	4	US-10-356-257-18
20	87	97.8	15	4	US-10-356-257-19
21	87	97.8	24	4	US-10-639-076-43
22	87	97.8	24	4	US-10-639-076-44
23	86	96.6	13	4	US-10-639-076-5
24	86	96.6	15	4	US-10-356-257-20
25	86	96.6	15	4	US-10-356-257-27
26	86	96.6	15	4	US-10-356-257-28
27	86	96.6	24	4	US-10-639-076-45

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31	85	95.5	24	4	US-10-639-076-30	Sequence 30, Appl
32	84	94.4	15	4	US-10-356-257-8	Sequence 8, Appl
33	84	94.4	15	4	US-10-356-257-10	Sequence 10, Appl
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35	84	94.4	15	4	US-10-356-257-15	Sequence 15, Appl
36	84	94.4	15	4	US-10-356-257-26	Sequence 26, Appl
37	84	94.4	15	4	US-10-356-257-29	Sequence 29, Appl
38	84	94.4	15	4	US-10-356-257-30	Sequence 30, Appl
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56	82	92.1	20	4	US-10-639-076-95	Sequence 95, Appl
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68	79	88.8	22	4	US-10-639-076-60	Sequence 60, Appl
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70	79	88.8	24	4	US-10-639-076-49	Sequence 49, Appl
71	79	88.8	24	4	US-10-639-076-58	Sequence 58, Appl
72	78	87.6	15	4	US-10-356-257-5	Sequence 5, Appl
73	78	87.6	15	4	US-10-356-257-34	Sequence 34, Appl
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75	78	87.6	18	4	US-10-639-076-79	Sequence 79, Appl
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84	76	85.4	15	4	US-10-356-257-22	Sequence 22, Appl
85	76	85.4	15	4	US-10-356-257-25	Sequence 25, Appl
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87	76	85.4	20	4	US-10-639-076-72	Sequence 72, Appl
88	76	85.4	24	4	US-10-639-076-47	Sequence 47, Appl
89	76	85.4	24	4	US-10-639-076-50	Sequence 50, Appl
90	75	84.3	13	4	US-10-639-076-25	Sequence 25, Appl
91	75	84.3	15	4	US-10-356-257-9	Sequence 9, Appl
92	75	84.3	15	4	US-10-356-257-11	Sequence 11, Appl
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94	75	84.3	24	4	US-10-639-076-32	Sequence 32, Appl
95	75	84.3	24	4	US-10-639-076-34	Sequence 34, Appl
96	74	83.1	20	4	US-10-639-076-70	Sequence 70, Appl
97	73	82.0	12	4	US-10-639-076-9	Sequence 9, Appl
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102	73	82.0	15	4	US-10-356-257-2	Sequence 2, Appli	175	43.5	48.9	21	4	US-10-158-825-30	Sequence 30, Appli
103	73	82.0	20	4	US-10-639-076-2	Sequence 2, Appli	176	43.5	48.9	118	4	US-10-162-335-26	Sequence 26, Appli
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108	73	82.0	20	4	US-10-639-076-90	Sequence 90, Appli	181	43.5	48.9	239	4	US-10-620-242A-24	Sequence 24, Appli
109	73	82.0	20	4	US-10-639-076-93	Sequence 93, Appli	182	43	48.3	15	5	US-10-920-244A-44	Sequence 44, Appli
110	72	80.9	13	4	US-10-639-076-84	Sequence 84, Appli	183	43	48.3	15	5	US-10-920-244A-192	Sequence 192, App
111	72	80.9	13	4	US-10-639-076-86	Sequence 86, Appli	184	43	48.3	54	3	US-09-843-676-183	Sequence 183, App
112	72	80.9	18	4	US-10-639-076-81	Sequence 81, Appli	185	43	48.3	54	3	US-09-438-486-183	Sequence 183, App
113	72	80.9	20	4	US-10-639-076-1	Sequence 1, Appli	186	43	48.3	54	4	US-10-053-758-183	Sequence 183, App
114	72	80.9	20	4	US-10-639-076-71	Sequence 71, Appli	187	43	48.3	54	4	US-10-054-295-183	Sequence 183, App
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117	71	79.8	13	4	US-10-639-076-22	Sequence 22, Appli	190	43	48.3	54	5	US-10-877-124-302	Sequence 302, App
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119	71	79.8	20	4	US-10-639-076-66	Sequence 66, Appli	192	43	48.3	54	5	US-10-877-146-302	Sequence 302, App
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122	68	76.4	20	4	US-10-639-076-96	Sequence 96, Appli	195	43	48.3	133	4	US-10-424-599-281240	Sequence 281240, A
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134	57	64.0	10	4	US-10-639-076-11	Sequence 11, Appli	207	43	48.3	458	4	US-10-116-688-4	Sequence 4, Appli
135	54	60.7	8	4	US-10-639-076-14	Sequence 14, Appli	208	43	48.3	458	6	US-11-116-760-4	Sequence 4, Appli
136	50	56.2	566	4	US-10-369-493-12517	Sequence 12517, A	209	43	48.3	521	4	US-10-686-947-216	Sequence 216, App
137	49	55.1	8	4	US-10-639-076-12	Sequence 12, Appli	210	43	48.3	521	4	US-10-686-947-264	Sequence 264, App
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139	49	55.1	533	5	US-10-739-930-5651	Sequence 5651, Ap	212	43	48.3	521	5	US-10-943-507-259	Sequence 259, App
140	47	52.8	27	5	US-10-794-514A-19	Sequence 19, Appli	213	43	48.3	1084	5	US-10-437-963-142768	Sequence 142768, A
141	47	52.8	27	5	US-10-794-514A-38	Sequence 38, Appli	214	43	48.3	1428	4	US-10-794-514A-336	Sequence 336, App
142	47	52.8	97	4	US-10-425-115-1286749	Sequence 286749, A	215	43	48.3	1428	4	US-10-275-107-54	Sequence 54, Appli
143	47	52.8	132	4	US-10-437-963-1782824	Sequence 1782824, A	216	42.5	47.8	226	4	US-10-282-122A-48140	Sequence 48140, A
144	47	52.8	469	4	US-10-437-963-130625	Sequence 130625, A	217	42.5	47.8	750	6	US-11-004-418A-32	Sequence 32, Appli
145	47	52.8	1167	5	US-10-794-514A-328	Sequence 328, App	218	42	47.2	13	4	US-10-158-847-103	Sequence 103, App
146	46	51.7	75	4	US-10-425-115-340523	Sequence 340523, A	219	42	47.2	13	4	US-10-158-825-103	Sequence 103, App
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159	44	49.4	98	4	US-10-424-599-240412	Sequence 240412, A	232	42	47.2	276	4	US-10-295-027-216	Sequence 216, App
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161	44	49.4	102	3	US-09-902-941-1818	Sequence 902-941-1818	234	42	47.2	328	3	US-09-922-364A-27	Sequence 27, Appli
162	44	49.4	102	3	US-09-849-626-1818	Sequence 1818, Ap	235	42	47.2	328	3	US-09-254-590-27	Sequence 27, Appli
163	44	49.4	102	3	US-09-374-046A-120	Sequence 120, App	236	42	47.2	328	4	US-10-115-695-27	Sequence 27, Appli
164	44	49.4	102	4	US-10-017-754-1818	Sequence 1818, Ap	237	42	47.2	328	4	US-10-116-561-27	Sequence 27, Appli
165	44	49.4	102	4	US-10-113-872-1818	Sequence 1818, Ap	238	42	47.2	328	4	US-10-115-671-27	Sequence 27, Appli
166	44	49.4	102	4	US-10-283-017-1818	Sequence 1818, Ap	239	42	47.2	328	4	US-10-115-415-27	Sequence 27, Appli
167	44	49.4	102	4	US-10-616-263-120	Sequence 120, App	240	42	47.2	328	4	US-10-116-260-27	Sequence 27, Appli
168	44	49.4	139	4	US-10-425-114-52714	Sequence 52714, A	241	42	47.2	328	4	US-10-115-688-27	Sequence 27, Appli
169	44	49.4	597	4	US-10-425-114-55831	Sequence 55831, A	242	42	47.2	328	6	US-11-116-760-27	Sequence 27, Appli
170	43.5	48.9	13	4	US-10-158-847-101	Sequence 101, App	243	42	47.2	553	3	US-09-922-364A-3	Sequence 3, Appli
171	43.5	48.9	13	4	US-10-158-825-101	Sequence 101, App	244	42	47.2	553	3	US-09-254-590-3	Sequence 3, Appli
172	43.5	48.9	13	4	US-10-158-825-101	Sequence 101, App	245	42	47.2	553	4	US-10-115-695-3	Sequence 3, Appli
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248	42	47.2	553	4	US-10-115-415-3	Sequence 3, Appli	321	41	46.1	49	4	US-10-424-599-170142	Sequence 170142,
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256	42	47.2	557	4	US-10-116-561-20	Sequence 20, Appl	329	41	46.1	122	4	US-10-424-599-143617	Sequence 143617,
257	42	47.2	557	4	US-10-115-671-20	Sequence 20, Appl	330	41	46.1	130	4	US-10-437-963-141077	Sequence 141077,
257	42	47.2	557	4	US-10-115-415-20	Sequence 20, Appl	331	41	46.1	141	5	US-10-450-763-37801	Sequence 37801, A
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262	42	47.2	561	3	US-09-254-590-1	Sequence 1, Appli	336	41	46.1	199	4	US-10-425-115-317525	Sequence 317525,
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269	42	47.2	561	6	US-11-116-760-1	Sequence 1, Appli	343	41	46.1	423	4	US-10-382-844-38	Sequence 38, Appl
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271	42	47.2	579	3	US-09-254-590-19	Sequence 19, Appl	345	41	46.1	458	5	US-10-943-507-278	Sequence 278, App
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275	42	47.2	579	4	US-10-115-415-19	Sequence 19, Appl	349	41	46.1	497	4	US-10-437-963-111779	Sequence 278, App
276	42	47.2	579	4	US-10-116-260-19	Sequence 19, Appl	350	41	46.1	516	4	US-10-686-947-278	Sequence 120513,
277	42	47.2	579	4	US-10-115-688-19	Sequence 19, Appl	351	41	46.1	563	4	US-10-437-963-120513	Sequence 9387, Ap
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279	42	47.2	579	4	US-10-295-027-596	Sequence 596, App	353	41	46.1	615	4	US-10-627-476-534	Sequence 536, App
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281	42	47.2	580	3	US-11-116-760-19	Sequence 19, Appl	355	41	46.1	624	4	US-10-424-599-208782	Sequence 208782,
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283	42	47.2	580	3	US-09-254-590-2	Sequence 2, Appli	357	41	46.1	860	4	US-10-424-599-208782	Sequence 208782,
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287	42	47.2	580	4	US-10-115-415-2	Sequence 2, Appli	361	41	46.1	1146	4	US-10-128-714-3444	Sequence 3444, App
288	42	47.2	580	4	US-10-116-260-2	Sequence 2, Appli	362	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
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294	42	47.2	732	4	US-09-254-590-43	Sequence 43, Appl	368	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
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298	42	47.2	732	4	US-10-115-415-43	Sequence 43, Appl	372	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
299	42	47.2	732	4	US-10-116-260-43	Sequence 43, Appl	373	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
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302	42	47.2	736	3	US-09-254-590-47	Sequence 47, Appl	376	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
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307	42	47.2	736	4	US-10-116-260-47	Sequence 47, Appl	381	40.5	45.5	106	4	US-10-128-714-3444	Sequence 3444, App
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397	40	44.9	202	4	US-10-023-386-33704	Sequence 33704, A	470	39	43.8	104	4	US-10-221-278-575	Sequence 575, App
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405	40	44.9	299	4	US-10-156-761-9607	Sequence 9607, Ap	478	39	43.8	172	4	US-10-108-260A-4704	Sequence 4704, Ap
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413	40	44.9	450	5	US-10-928-992-54	Sequence 54, Appl	486	39	43.8	269	3	US-09-978-360A-529	Sequence 529, App
414	40	44.9	469	4	US-10-425-115-326803	Sequence 326803, Ap	487	39	43.8	283	4	US-10-424-599-243056	Sequence 243056,
415	40	44.9	539	3	US-09-810-927B-3	Sequence 3, Appli	488	39	43.8	308	5	US-10-732-923-2426	Sequence 2426, Ap
416	40	44.9	564	5	US-10-481-032A-314	Sequence 314, App	489	39	43.8	308	5	US-10-732-923-2427	Sequence 2427, Ap
417	40	44.9	810	3	US-09-809-567-3	Sequence 3, Appli	490	39	43.8	308	5	US-10-732-923-2428	Sequence 2428, Ap
418	40	44.9	810	4	US-10-216-156-3	Sequence 3, Appli	491	39	43.8	317	5	US-10-732-923-2961	Sequence 2961, Ap
419	40	44.9	866	3	US-10-616-788-3	Sequence 3, Appli	492	39	43.8	319	4	US-10-282-122A-46224	Sequence 46224, A
420	40	44.9	866	3	US-09-778-971-9	Sequence 9, Appli	493	39	43.8	322	4	US-10-437-963-152254	Sequence 152254,
421	40	44.9	866	4	US-10-033-522-1	Sequence 1, Appli	494	39	43.8	330	4	US-10-309-515-39	Sequence 39, Appl
422	40	44.9	866	4	US-10-207-655-107	Sequence 107, App	495	39	43.8	330	4	US-10-291-990-7	Sequence 7, Appl
423	40	44.9	866	4	US-10-742-161-10	Sequence 10, Appl	496	39	43.8	330	4	US-10-291-990-17	Sequence 17, Appl
424	40	44.9	866	4	US-10-742-372-10	Sequence 10, Appl	497	39	43.8	330	4	US-10-291-990-18	Sequence 18, Appl
425	40	44.9	866	4	US-10-646-308-4	Sequence 4, Appli	498	39	43.8	330	4	US-10-126-764-39	Sequence 39, Appl
426	40	44.9	866	5	US-10-918-084-1	Sequence 9, Appli	499	39	43.8	330	4	US-10-478-534-1	Sequence 1, Appli
427	40	44.9	900	4	US-11-128-403-9	Sequence 9, Appli	500	39	43.8	335	4	US-10-333-946-11	Sequence 11, Appl
428	40	44.9	900	4	US-10-374-979-91	Sequence 91, Appl	501	39	43.8	340	3	US-09-791-932-117	Sequence 117, App
429	40	44.9	900	4	US-10-182-936A-91	Sequence 91, Appl	502	39	43.8	340	3	US-09-990-940-2	Sequence 2, Appli
430	40	44.9	900	5	US-10-477-238A-670	Sequence 670, App	503	39	43.8	340	3	US-09-964-923A-2	Sequence 4, Appli
431	40	44.9	900	5	US-10-680-287A-670	Sequence 670, App	504	39	43.8	340	3	US-09-971-269-4	Sequence 666, App
432	40	44.9	900	5	US-10-477-173-670	Sequence 670, App	505	39	43.8	340	4	US-10-225-567A-666	Sequence 34, Appl
433	40	44.9	912	4	US-10-092-900A-270	Sequence 270, App	506	39	43.8	340	4	US-10-309-515-34	Sequence 34, Appl
434	40	44.9	1080	4	US-10-282-942-2	Sequence 2, Appli	507	39	43.8	340	4	US-10-309-515-36	Sequence 36, Appl
435	40	44.9	1080	5	US-10-745-237-248	Sequence 248, App	508	39	43.8	340	4	US-10-291-990-2	Sequence 2, Appli
436	40	44.9	1080	5	US-10-745-237-302	Sequence 302, App	509	39	43.8	340	4	US-10-291-990-22	Sequence 22, Appl
437	40	44.9	1207	5	US-10-732-923-8227	Sequence 8227, Ap	510	39	43.8	340	4	US-10-291-990-24	Sequence 24, Appl
438	40	44.9	1887	4	US-10-437-963-107783	Sequence 107783, Ap	511	39	43.8	340	4	US-10-291-990-26	Sequence 26, Appl
439	39.5	44.4	18	3	US-09-858-935B-121	Sequence 121, App	512	39	43.8	340	4	US-10-291-990-29	Sequence 29, Appl
440	39.5	44.4	18	4	US-10-271-869-121	Sequence 121, App	513	39	43.8	340	4	US-10-321-807-40	Sequence 40, Appl
441	39.5	44.4	41	4	US-10-424-599-275353	Sequence 275353, Ap	514	39	43.8	340	4	US-10-126-764-34	Sequence 34, Appl
442	39.5	44.4	55	4	US-10-425-115-262510	Sequence 262510, Ap	515	39	43.8	340	4	US-10-126-764-36	Sequence 36, Appl
443	39.5	44.4	104	4	US-10-016-634A-174	Sequence 174, App	516	39	43.8	340	4	US-10-332-082-3	Sequence 3, Appli
444	39.5	44.4	128	4	US-10-425-115-268283	Sequence 268283, Ap	517	39	43.8	340	4	US-10-332-082-3	Sequence 3, Appli
445	39.5	44.4	149	4	US-10-425-115-285303	Sequence 285303, Ap	518	39	43.8	340	4	US-10-472-629-3	Sequence 2, Appli
446	39.5	44.4	165	4	US-10-156-761-12033	Sequence 12033, A	519	39	43.8	340	4	US-10-478-534-2	Sequence 3, Appli
447	39.5	44.4	213	4	US-10-425-115-254699	Sequence 254699, Ap	520	39	43.8	340	4	US-10-478-534-3	Sequence 4, Appli
448	39.5	44.4	422	5	US-10-450-763-52205	Sequence 52205, A	521	39	43.8	340	4	US-10-126-764-34	Sequence 34, Appl
449	39.5	44.4	547	4	US-10-032-585-7584	Sequence 7584, Ap	522	39	43.8	340	4	US-10-126-764-36	Sequence 36, Appl
450	39	43.8	7	4	US-10-714-564A-223	Sequence 223, App	523	39	43.8	340	4	US-10-321-807-40	Sequence 40, Appl
451	39	43.8	13	4	US-10-158-847-112	Sequence 112, App	524	39	43.8	340	4	US-10-314-048A-40	Sequence 40, Appl
452	39	43.8	13	4	US-10-158-825-112	Sequence 112, App	525	39	43.8	340	4	US-10-477-985-58	Sequence 58, Appl
453	39	43.8	30	5	US-10-792-582-165	Sequence 165, App	526	39	43.8	340	5	US-10-680-402-2	Sequence 2, Appli
454	39	43.8	31	4	US-10-363-204-125	Sequence 125, App	527	39	43.8	340	5	US-10-500-672-37	Sequence 37, Appl
455	39	43.8	31	5	US-10-784-537-1	Sequence 1, Appli	528	39	43.8	340	5	US-10-941-486-5	Sequence 5, Appli
456	39	43.8	31	5	US-10-784-537-9	Sequence 9, Appli	529	39	43.8	340	5	US-10-930-662-40	Sequence 40, Appl
457	39	43.8	35	4	US-10-424-599-191548	Sequence 191548, Ap	530	39	43.8	340	6	US-11-038-360-2	Sequence 2, Appli
458	39	43.8	57	4	US-10-424-599-256821	Sequence 256821, Ap	531	39	43.8	346	4	US-10-291-990-21	Sequence 21, Appl
459	39	43.8	58	4	US-10-424-599-256821	Sequence 256821, Ap	532	39	43.8	346	4	US-10-291-990-23	Sequence 23, Appl
460	39	43.8	59	4	US-10-425-115-261891	Sequence 261891, Ap	533	39	43.8	346	4	US-10-291-990-33	Sequence 33, Appl
461	39	43.8	59	4	US-10-424-599-234470	Sequence 234470, Ap	534	39	43.8	348	4	US-10-291-990-33	Sequence 33, Appl
462	39	43.8	60	4	US-10-425-115-358505	Sequence 358505, Ap	535	39	43.8	348	4	US-10-291-990-15	Sequence 15, Appl
463	39	43.8	64	4	US-10-178-213-299	Sequence 299, App	536	39	43.8	348	4	US-10-291-990-16	Sequence 16, Appl
464	39	43.8	70	4	US-10-424-599-204062	Sequence 204062, Ap	537	39	43.8	359	4	US-10-309-515-50	Sequence 50, Appl
465	39	43.8	75	4	US-10-424-599-235742	Sequence 235742, Ap	538	39	43.8	364	4	US-10-126-764-50	Sequence 50, Appl
466	39	43.8	76	4	US-10-425-115-317741	Sequence 317741, Ap	539	39	43.8	364	4	US-10-424-599-1	Sequence 176823,

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542	39	43.8	398	5	US-10-450-763-59224	Sequence 59224, A	615	38	42.7	95	4	US-10-623-500-4	Sequence 4, Appl
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544	39	43.8	443	5	US-10-437-963-23766	Sequence 23766, A	617	38	42.7	96	4	US-10-424-599-284212	Sequence 284212, A
545	39	43.8	445	4	US-10-264-237-1646	Sequence 1646, A	618	38	42.7	96	4	US-10-425-115-201385	Sequence 201385, A
546	39	43.8	459	4	US-10-239-704-2	Sequence 2, Appl	619	38	42.7	96	4	US-10-425-115-286866	Sequence 286866, A
547	39	43.8	472	4	US-10-369-493-22804	Sequence 22804, A	620	38	42.7	97	4	US-10-424-599-203966	Sequence 203966, A
548	39	43.8	540	4	US-10-437-963-171694	Sequence 171694, A	621	38	42.7	98	4	US-10-424-599-203379	Sequence 203379, A
549	39	43.8	548	4	US-10-437-963-171694	Sequence 171694, A	622	38	42.7	98	4	US-10-425-115-37343	Sequence 37343, A
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551	39	43.8	782	4	US-10-425-115-18716	Sequence 18716, A	624	38	42.7	100	5	US-10-504-582-93	Sequence 582-93, A
552	39	43.8	865	4	US-10-437-963-142919	Sequence 142919, A	625	38	42.7	102	4	US-10-425-114-45175	Sequence 45175, A
553	39	43.8	868	5	US-10-450-763-50930	Sequence 50930, A	626	38	42.7	102	4	US-10-767-701-37437	Sequence 37437, A
554	39	43.8	874	5	US-10-450-763-56467	Sequence 56467, A	627	38	42.7	107	4	US-10-425-115-199818	Sequence 199818, A
555	39	43.8	897	5	US-10-450-763-46300	Sequence 46300, A	628	38	42.7	111	4	US-10-425-115-366241	Sequence 366241, A
556	39	43.8	1024	4	US-10-211-962-63	Sequence 83, Appl	629	38	42.7	125	4	US-10-437-963-125780	Sequence 125780, A
557	39	43.8	1078	6	US-11-097-143-10548	Sequence 10548, A	630	38	42.7	135	4	US-10-425-114-40528	Sequence 40528, A
558	39	43.8	1162	5	US-10-450-763-35411	Sequence 35411, A	631	38	42.7	135	5	US-10-450-763-57919	Sequence 57919, A
559	39	43.8	1253	5	US-10-205-219-106	Sequence 106, App	632	38	42.7	136	4	US-10-108-2608-3751	Sequence 3751, A
560	39	43.8	1829	5	US-10-732-923-8687	Sequence 8687, App	633	38	42.7	136	5	US-10-450-763-43114	Sequence 43114, A
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563	38.5	43.3	90	4	US-10-424-599-217679	Sequence 217679, A	636	38	42.7	152	3	US-09-736-457-787	Sequence 787, App
564	38.5	43.3	138	4	US-10-425-115-190607	Sequence 190607, A	637	38	42.7	152	3	US-09-736-457-795	Sequence 795, App
565	38.5	43.3	154	4	US-10-425-115-270230	Sequence 270230, A	638	38	42.7	152	3	US-09-902-941-787	Sequence 787, App
566	38.5	43.3	186	4	US-10-204-887-129	Sequence 129, App	639	38	42.7	152	3	US-09-902-941-795	Sequence 795, App
567	38.5	43.3	189	4	US-10-424-599-209967	Sequence 209967, A	640	38	42.7	152	3	US-09-849-626-795	Sequence 795, App
568	38.5	43.3	488	3	US-09-563-728A-26	Sequence 26, Appl	641	38	42.7	152	3	US-09-849-626-795	Sequence 795, App
569	38.5	43.3	488	4	US-10-177-293-206	Sequence 206, App	642	38	42.7	152	4	US-10-017-754-787	Sequence 787, App
570	38.5	43.3	488	4	US-10-360-534-2	Sequence 2, Appl	643	38	42.7	152	4	US-10-017-754-795	Sequence 795, App
571	38.5	43.3	488	5	US-10-723-860-2984	Sequence 2984, App	644	38	42.7	152	4	US-10-113-872-787	Sequence 787, App
572	38.5	43.3	488	5	US-10-941-947-6	Sequence 6, Appl	645	38	42.7	152	4	US-10-113-872-795	Sequence 795, App
573	38.5	43.3	489	3	US-09-817-913-3	Sequence 3, Appl	646	38	42.7	152	4	US-10-283-017-787	Sequence 787, App
574	38.5	43.3	489	3	US-09-817-538-3	Sequence 3, Appl	647	38	42.7	152	4	US-10-283-017-795	Sequence 795, App
575	38.5	43.3	489	5	US-10-870-587-3	Sequence 3, Appl	648	38	42.7	154	4	US-10-425-115-229623	Sequence 229623, A
576	38.5	43.3	498	5	US-10-803-575B-3	Sequence 3, Appl	649	38	42.7	155	3	US-09-925-299-1123	Sequence 1123, Ap
577	38.5	43.3	498	5	US-10-803-344B-3	Sequence 3, Appl	650	38	42.7	155	3	US-09-925-299-1123	Sequence 1123, Ap
578	38.5	43.3	498	5	US-10-803-580B-3	Sequence 3, Appl	651	38	42.7	155	3	US-09-925-299-1123	Sequence 1123, Ap
579	38.5	43.3	498	6	US-11-013-234-3	Sequence 3, Appl	652	38	42.7	165	3	US-09-942-052-706	Sequence 706, App
580	38.5	43.3	498	6	US-11-013-056-3	Sequence 3, Appl	653	38	42.7	165	3	US-10-437-963-115705	Sequence 115705, A
581	38.5	43.3	1011	4	US-10-389-566-1907	Sequence 1907, Ap	654	38	42.7	174	4	US-10-437-963-194553	Sequence 194553, A
582	38.5	43.3	1737	4	US-10-263-929-195	Sequence 195, App	655	38	42.7	177	4	US-10-425-115-306601	Sequence 306601, A
583	38.5	43.3	1774	4	US-10-466-720-6	Sequence 6, Appl	656	38	42.7	179	4	US-10-223-047-11	Sequence 11, Appl
584	38.5	43.3	2854	4	US-10-085-198-16	Sequence 16, Appl	657	38	42.7	187	4	US-10-101-464A-732	Sequence 732, App
585	38	42.7	7	4	US-10-714-564A-230	Sequence 230, App	658	38	42.7	187	5	US-10-864-252-732	Sequence 732, App
586	38	42.7	7	4	US-10-714-564A-230	Sequence 230, App	659	38	42.7	189	4	US-10-437-963-121175	Sequence 121175, A
587	38	42.7	20	3	US-09-962-756-396	Sequence 996, App	660	38	42.7	200	4	US-10-424-599-280188	Sequence 280188, A
588	38	42.7	20	4	US-10-253-471-396	Sequence 996, App	661	38	42.7	206	4	US-10-425-115-210928	Sequence 210928, A
589	38	42.7	20	4	US-10-253-493-396	Sequence 996, App	662	38	42.7	214	4	US-10-123-965B-4	Sequence 4, Appl
590	38	42.7	34	3	US-09-864-761-45579	Sequence 45579, A	663	38	42.7	214	5	US-10-779-304-4	Sequence 4, Appl
591	38	42.7	39	4	US-10-424-599-262999	Sequence 262999, A	664	38	42.7	214	5	US-10-985-804-3	Sequence 3, Appl
592	38	42.7	48	4	US-10-185-050-72	Sequence 72, Appl	665	38	42.7	215	4	US-10-225-066A-216	Sequence 216, App
593	38	42.7	49	3	US-09-864-761-33649	Sequence 33649, A	666	38	42.7	215	4	US-10-374-780A-2454	Sequence 2454, Ap
594	38	42.7	49	4	US-10-029-386-30004	Sequence 30004, A	667	38	42.7	215	5	US-10-985-804-5	Sequence 5, Appl
595	38	42.7	60	5	US-10-450-763-40245	Sequence 40245, A	668	38	42.7	215	5	US-10-225-066A-216	Sequence 4, Appl
596	38	42.7	69	4	US-10-425-115-286671	Sequence 286671, A	669	38	42.7	216	5	US-10-985-804-4	Sequence 4, Appl
597	38	42.7	70	5	US-10-424-599-374947	Sequence 374947, A	670	38	42.7	228	4	US-10-104-047-2899	Sequence 2829, Ap
598	38	42.7	70	4	US-10-499-353A-500	Sequence 500, App	671	38	42.7	228	4	US-10-282-122A-47880	Sequence 47880, A
599	38	42.7	74	4	US-10-425-115-292434	Sequence 292434, A	672	38	42.7	246	4	US-10-437-963-115701	Sequence 115701, A
600	38	42.7	74	4	US-10-425-115-320584	Sequence 320584, A	673	38	42.7	262	5	US-10-425-115-230479	Sequence 230479, A
601	38	42.7	76	5	US-10-450-763-37117	Sequence 37117, A	674	38	42.7	262	5	US-10-739-930-5779	Sequence 5779, Ap
602	38	42.7	79	4	US-10-106-698-4310	Sequence 4310, Ap	675	38	42.7	262	5	US-10-171-844-2	Sequence 2, Appl
603	38	42.7	81	3	US-09-805-204-10	Sequence 10, Appl	676	38	42.7	262	5	US-10-424-599-189338	Sequence 189338, A
604	38	42.7	81	4	US-10-103-511-10	Sequence 10, Appl	677	38	42.7	275	4	US-10-437-963-108816	Sequence 108816, A
605	38	42.7	82	4	US-10-425-115-342158	Sequence 342158, A	678	38	42.7	275	4	US-10-424-599-236429	Sequence 236429, A
606	38	42.7	87	4	US-10-424-599-168009	Sequence 168009, A	679	38	42.7	302	5	US-10-739-930-6550	Sequence 6550, Ap
607	38	42.7	90	4	US-10-243-552-868	Sequence 868, App	680	38	42.7	304	5	US-10-686-947-286	Sequence 286, App
608	38	42.7	90	4	US-10-623-500-6	Sequence 6, Appl	681	38	42.7	304	5	US-10-943-507-286	Sequence 286, App
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610	38	42.7	90	4	US-10-425-115-342161	Sequence 342161, A	683	38	42.7	323	4	US-10-177-293-6	Sequence 6, Appl
611	38	42.7	90	5	US-10-450-763-48299	Sequence 48299, A	684	38	42.7	323	4	US-10-321-204-17	Sequence 17, Appl

685	38	42.7	323	4	US-10-321-204-33	Sequence 33, Appl	758	38	42.7	1215	4	US-10-360-534-6	Sequence 6, Appl
686	38	42.7	323	4	US-10-321-204-34	Sequence 34, Appl	759	38	42.7	1215	5	US-10-870-587-11	Sequence 11, Appl
687	38	42.7	323	4	US-10-648-593-152	Sequence 152, Appl	760	38	42.7	1363	4	US-10-437-963-176022	Sequence 176022,
688	38	42.7	323	4	US-10-476-033-3	Sequence 3, Appl	761	38	42.7	1394	4	US-10-101-388-3	Sequence 3, Appl
689	38	42.7	323	5	US-10-723-860-918	Sequence 918, Appl	762	38	42.7	1402	4	US-10-795-931-9	Sequence 9, Appl
690	38	42.7	323	5	US-10-772-636-2	Sequence 2, Appl	763	38	42.7	1406	4	US-10-437-963-143009	Sequence 143009,
691	38	42.7	323	5	US-10-631-467-828	Sequence 828, Appl	764	38	42.7	1504	6	US-11-097-143-7866	Sequence 7866, Ap
692	38	42.7	325	5	US-10-756-145-4942	Sequence 4942, Ap	765	38	42.7	1620	5	US-10-745-237-200	Sequence 200, App
693	38	42.7	330	4	US-10-236-055A-6	Sequence 6, Appl	766	38	42.7	2066	4	Sequence 176144,	Sequence 176144,
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695	38	42.7	331	4	US-10-220-120-354	Sequence 354, Appl	768	38	42.7	2496	4	US-10-437-963-171380	Sequence 171380,
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707	38	42.7	480	4	US-10-080-170-638	Sequence 638, Appl	780	37.5	42.1	124	4	US-10-425-115-34358	Sequence 34358,
708	38	42.7	480	4	US-10-468-356-638	Sequence 638, Appl	781	37.5	42.1	243	5	US-10-450-763-47863	Sequence 47863, A
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710	38	42.7	481	3	US-09-817-464-8	Sequence 8, Appl	783	37.5	42.1	308	5	US-10-490-318-19	Sequence 19, Appl
711	38	42.7	481	4	US-10-331-289-8	Sequence 8, Appl	784	37.5	42.1	743	5	US-10-618-281-75	Sequence 75, Appl
712	38	42.7	481	4	US-10-238-075-1333	Sequence 1333, Ap	785	37.5	42.1	752	4	US-10-437-963-173605	Sequence 173605,
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987 37 41.6 513 4 US-10-140-808-536
988 37 41.6 513 4 US-10-063-569-124
989 37 41.6 513 4 US-10-063-513-124
990 37 41.6 513 4 US-10-063-513-124
991 37 41.6 513 4 US-10-063-512-124
992 37 41.6 513 4 US-10-121-049-536
993 37 41.6 513 4 US-10-123-904-536
994 37 41.6 513 4 US-10-140-470-536
995 37 41.6 513 4 US-10-063-502-124
996 37 41.6 513 4 US-10-175-746-536
997 37 41.6 513 4 US-10-176-918-536
998 37 41.6 513 4 US-10-176-921-536
999 37 41.6 513 4 US-10-063-549-124
1000 37 41.6 513 4 US-10-137-865-536

ALIGNMENTS

RESULT 1
US-10-639-076-4
; Sequence 4, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-4

Query Match 100.0%; Score 89; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13

RESULT 2
US-10-356-257-40
; Sequence 40, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257

; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 40
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-40

Query Match 100.0%; Score 89; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13

RESULT 3
US-10-639-076-23
; Sequence 23, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-23

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 4
US-10-356-257-3
; Sequence 3, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
US-10-356-257-3

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-3

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| | | | | | | | | | | | | | |
Db 3 WEVLCWTWETCER 15

RESULT 5
US-10-356-257-4
; Sequence 4, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: Fv11a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-4

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| | | | | | | | | | | | | | |
Db 3 WEVLCWTWETCER 15

RESULT 6
US-10-356-257-16
; Sequence 16, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: Fv11a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-16

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| | | | | | | | | | | | | | |
Db 3 WEVLCWTWETCER 15

RESULT 7
US-10-356-257-32
; Sequence 32, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: Fv11a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-32

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| | | | | | | | | | | | | | |
Db 1 WEVLCWTWETCER 13

RESULT 8
US-10-639-076-17
; Sequence 17, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Fv11a Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 17
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-17

Query Match 100.0%; Score 89; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
| | | | | | | | | | | | | | |
Db 2 WEVLCWTWETCER 14

RESULT 9
US-10-639-076-18
; Sequence 18, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis

```
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-18

Query Match      100.0%; Score 89; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 10
US-10-639-076-57
; Sequence 57, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 57
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-57

Query Match      100.0%; Score 89; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      1 WEVLCWTWETCER 13

RESULT 11
US-10-639-076-19
; Sequence 19, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
```

```
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 19
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-19

Query Match      100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 12
US-10-639-076-26
; Sequence 26, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 26
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-26

Query Match      100.0%; Score 89; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 13
US-10-639-076-27
; Sequence 27, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
```

; NUMBER OF SEQ ID NOS: 100

; SEQ ID NO 27

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide sequence

US-10-639-076-27

Query Match 100.0%; Score 89; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13

Db 3 WEVLCWTWETCER 15

RESULT 14

US-10-639-076-39

; Sequence 39, Application US/10639076

; Publication No. US20040077547A1

; GENERAL INFORMATION:

; APPLICANT: Mark S. Dennis

; TITLE OF INVENTION: FVIIa Antagonists

; CURRENT APPLICATION NUMBER: US/10/639,076

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: US/09/632,429

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/147,627

; PRIOR FILING DATE: 1999-08-06

; PRIOR APPLICATION NUMBER: US 60/150,315

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 100

; SEQ ID NO 39

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide sequence

US-10-639-076-39

Query Match 100.0%; Score 89; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13

Db 3 WEVLCWTWETCER 15

RESULT 15

US-10-639-076-40

; Sequence 40, Application US/10639076

; Publication No. US20040077547A1

; GENERAL INFORMATION:

; APPLICANT: Mark S. Dennis

; TITLE OF INVENTION: FVIIa Antagonists

; CURRENT APPLICATION NUMBER: US/10/639,076

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: US/09/632,429

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/147,627

; PRIOR FILING DATE: 1999-08-06

; PRIOR APPLICATION NUMBER: US 60/150,315

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 100

; SEQ ID NO 40

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide sequence

US-10-639-076-40

Query Match 100.0%; Score 89; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13

Db 3 WEVLCWTWETCER 15

RESULT 16

US-10-639-076-41

; Sequence 41, Application US/10639076

; Publication No. US20040077547A1

; GENERAL INFORMATION:

; APPLICANT: Mark S. Dennis

; TITLE OF INVENTION: FVIIa Antagonists

; CURRENT APPLICATION NUMBER: US/10/639,076

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: US/09/632,429

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/147,627

; PRIOR FILING DATE: 1999-08-06

; PRIOR APPLICATION NUMBER: US 60/150,315

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 100

; SEQ ID NO 41

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide sequence

US-10-639-076-41

Query Match 100.0%; Score 89; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13

Db 3 WEVLCWTWETCER 15

RESULT 17

US-10-356-257-17

; Sequence 17, Application US/10356257

; Publication No. US20040087767A1

; GENERAL INFORMATION:

; APPLICANT: LAZARUS, ROBERT A.

; TITLE OF INVENTION: FVIIa Antagonists

; CURRENT APPLICATION NUMBER: US/10/356,257

; CURRENT FILING DATE: 2003-01-30

; PRIOR APPLICATION NUMBER: US 60/355,420

; PRIOR FILING DATE: 2002-02-06

; NUMBER OF SEQ ID NOS: 355

; SEQ ID NO 17

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

US-10-356-257-17

Query Match 98.9%; Score 88; DB 4; Length 15;

Best Local Similarity 92.3%; Pred. No. 0.0002;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 18
US-10-639-076-42
; Sequence 42, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 19
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-19

Query Match      97.8%; Score 87; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00027;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 21
US-10-639-076-43
; Sequence 43, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 43
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-43

Query Match      97.8%; Score 87; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00039;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 22
US-10-639-076-44
; Sequence 44, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
```

```
Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 18
US-10-639-076-42
; Sequence 42, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 42
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-42

Query Match      98.9%; Score 88; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00029;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 19
US-10-356-257-18
; Sequence 18, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 18
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-18

Query Match      97.8%; Score 87; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00027;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCER 13
Db      3 WEVLCWTWETCER 15

RESULT 20
US-10-356-257-19
; Sequence 19, Application US/10356257
```

; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 44
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-44

Query Match 97.8%; Score 87; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00039; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 23
US-10-639-076-5
; Sequence 5, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-5

Query Match 96.6%; Score 86; DB 4; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00032; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 1 WEVLCWTWETCER 13

RESULT 24
US-10-356-257-20
; Sequence 20, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 20
; LENGTH: 15

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-20

Query Match 96.6%; Score 86; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00035; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 25
US-10-356-257-27
; Sequence 27, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-27

Query Match 96.6%; Score 86; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00035; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 26
US-10-356-257-28
; Sequence 28, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-28

Query Match 96.6%; Score 86; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00035; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13

```
Db          |||||:
            3 WEVLCWTWETCEK 15

RESULT 27
US-10-639-076-45
; Sequence 45, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 45
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-45

Query Match          96.6%; Score 86; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00052;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-10-639-076-45
Qy      1 WEVLCWTWETCER 13
         |||||:
Db      3 WEVLCWTWETCEK 15

RESULT 28
US-10-639-076-52
; Sequence 52, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 52
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-52

Query Match          96.6%; Score 86; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00052;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-10-639-076-52
Qy      1 WEVLCWTWETCER 13
         |||||:
Db      3 WEVLCWTWETCEK 15

RESULT 29
US-10-639-076-53
; Sequence 53, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 53
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-53

Query Match          96.6%; Score 86; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00052;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

US-10-639-076-53
Qy      1 WEVLCWTWETCER 13
         |||||:
Db      3 WEVLCWTWETCEK 15

RESULT 30
US-10-356-257-7
; Sequence 7, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-7

Query Match          95.5%; Score 85; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00047;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-356-257-7
Qy      1 WEVLCWTWETCER 13
         |||||:
Db      3 WEVLCWTWETCEK 15

RESULT 31
US-10-639-076-30
; Sequence 30, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
```


; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 30
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-30

Query Match 95.5%; Score 85; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEALCWTWETCER 15
|||||

RESULT 32
US-10-356-257-8
; Sequence 8, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-8

Query Match 94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVACWTWETCER 15
|||||

RESULT 33
US-10-356-257-10
; Sequence 10, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-10

Query Match 94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWAWETCER 15
|||||

RESULT 34
US-10-356-257-13
; Sequence 13, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-13

Query Match 94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15
|||||

RESULT 35
US-10-356-257-15
; Sequence 15, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-15

Query Match 94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 12
|||||

```
Db          3 WEVLCWTWETCE 14

RESULT 36
US-10-356-257-26
; Sequence 26, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 26
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-26

Query Match          94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 WEVLCWTWETCER 13
           ||||| |||||
Db          3 WEVLCWTWETCER 15

RESULT 37
US-10-356-257-29
; Sequence 29, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-29

Query Match          94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 WEVLCWTWETCER 12
           ||||| |||||
Db          3 WEVLCWTWETCER 14

RESULT 38
US-10-356-257-30
; Sequence 30, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 30
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-30

Query Match          94.4%; Score 84; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 WEVLCWTWETCER 13
           ||||| |||||
Db          3 WEVLCWTWETCER 15

RESULT 39
US-10-639-076-31
; Sequence 31, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 31
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-31

Query Match          94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 WEVLCWTWETCER 13
           ||||| |||||
Db          3 WEVLCWTWETCER 15

RESULT 40
US-10-639-076-33
; Sequence 33, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
```

```
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 33
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-33

Query Match          94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WEVLCWTWETCER 13
        |||||
Db       3 WEVLCWAWETCER 15

RESULT 41
US-10-639-076-36
; Sequence 36, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 36
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-36

Query Match          94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WEVLCWTWETCER 13
        |||||
Db       3 WEVLCWAWETCER 15

RESULT 42
US-10-639-076-38
; Sequence 38, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 38
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
US-10-639-076-38

Query Match          94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WEVLCWTWETCER 13
        |||||
Db       3 WEVLCWAWETCER 15

RESULT 43
US-10-639-076-51
; Sequence 51, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 51
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-51

Query Match          94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 92.3%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 WEVLCWTWETCER 13
        |||||
Db       3 WEVLCWAWETCER 15

RESULT 44
US-10-639-076-54
; Sequence 54, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FVIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 54
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-54

Query Match          94.4%; Score 84; DB 4; Length 24;
```

```
Best Local Similarity 100.0%; Pred. No. 0.00092; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

Qy 1 WEVLCWTWETCE 12
    |||||
Db 3 WEVLCWTWETCE 14

RESULT 45
US-10-639-076-55
; Sequence 55, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 55
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-55

Query Match 94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCE 12
    |||||
Db 3 WEVLCWTWETCE 14

RESULT 46
US-10-639-076-65
; Sequence 65, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-65

Query Match 94.4%; Score 84; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCE 12
    |||||
Db 3 WEVLCWTWETCE 14

RESULT 47
US-10-639-076-3
; Sequence 3, Application US/10639076
; Publication No. US20040077547A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1639R1
; CURRENT APPLICATION NUMBER: US/10/639,076
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US/09/632,429
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/147,627
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: US 60/150,315
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-639-076-3

Query Match 93.3%; Score 83; DB 4; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.00075;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
    |||||
Db 1 WEVLCWTWEDCER 13

RESULT 48
US-10-356-257-6
; Sequence 6, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-6

Query Match 93.3%; Score 83; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00084;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEVLCWTWETCER 13
    |||||
Db 3 WAVLCWTWETCER 15

RESULT 49
US-10-356-257-12
; Sequence 12, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
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; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-12

Query Match 93.3%; Score 83; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00084;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCER 15

RESULT 50
US-10-356-257-14
; Sequence 14, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: FvIIa Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 14
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-14

Query Match 93.3%; Score 83; DB 4; Length 15;
Best Local Similarity 92.3%; Pred. No. 0.00084;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WEVLCWTWETCER 13
Db 3 WEVLCWTWETCAR 15

Search completed: March 28, 2006, 11:55:23
Job time : 178 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 28, 2006, 11:52:44 ; Search time 24 Seconds
(without alignments)
15.976 Million cell updates/sec

Title: US-10-639-076-4

Perfect score: 89

Sequence: 1 WEVLQWTWETCER 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:

- 1: /SIDSS/prodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /SIDSS/prodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /SIDSS/prodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /SIDSS/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 5: /SIDSS/prodata/1/pubpaa/US09_NEW_PUB.pep:*
- 6: /SIDSS/prodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /SIDSS/prodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /SIDSS/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	49.4	204	7	US-11-096-568A-23439
2	44	49.4	250	7	US-11-096-568A-23438
3	43	48.3	361	7	US-11-207-078-302
4	43	48.3	321	7	US-11-055-822-130
5	43	48.3	521	6	US-10-934-944-216
6	43	48.3	521	6	US-10-934-944-264
7	43	48.3	521	7	US-11-116-881A-225
8	43	48.3	521	7	US-11-116-881A-273
9	42.5	47.8	750	7	US-11-089-551A-22
10	42	47.2	405	7	US-11-096-568A-30667
11	42	47.2	438	7	US-11-096-568A-30666
12	42	47.2	447	7	US-11-096-568A-30665
13	42	47.2	579	6	US-10-975-798-4
14	42	47.2	580	6	US-10-975-798-3
15	42	47.2	731	6	US-10-613-744-10
16	41	46.1	231	7	US-11-009-658-6
17	41	46.1	296	7	US-11-096-568A-17867
18	41	46.1	458	6	US-10-934-944-284
19	41	46.1	458	7	US-11-116-881A-293
20	41	46.1	516	6	US-10-934-944-278
21	41	46.1	516	7	US-11-116-881A-287
22	40.5	45.5	106	7	US-11-000-463-750
23	40.5	45.5	106	7	US-11-000-463-751
24	40	44.9	256	7	US-11-096-568A-24137
25	40	44.9	271	7	US-11-098-686-10766

26	40	44.9	291	7	US-11-096-568A-24136	Sequence 24136, A
27	40	44.9	460	7	US-11-096-568A-24135	Sequence 24135, A
28	40	44.9	491	7	US-11-087-099-8792	Sequence 8792, Ap
29	40	44.9	900	6	US-10-501-035-215	Sequence 215, App
30	39	43.8	64	7	US-11-123-896-299	Sequence 299, App
31	39	43.8	192	7	US-11-096-568A-17129	Sequence 17129, A
32	39	43.8	269	5	US-09-978-360A-529	Sequence 529, App
33	39	43.8	273	7	US-11-096-568A-33844	Sequence 33844, A
34	39	43.8	287	7	US-11-096-568A-33843	Sequence 33843, A
35	39	43.8	302	7	US-11-096-568A-17128	Sequence 17128, A
36	39	43.8	308	7	US-11-096-568A-33842	Sequence 33842, A
37	39	43.8	340	6	US-10-980-388-117	Sequence 117, App
38	39	43.8	340	7	US-11-127-877-53	Sequence 53, Appl
39	39	43.8	353	7	US-11-096-568A-31101	Sequence 31101, A
40	39	43.8	396	7	US-11-096-568A-31100	Sequence 31100, A
41	39	43.8	399	7	US-11-096-568A-27975	Sequence 27975, A
42	39	43.8	399	7	US-11-096-568A-31099	Sequence 31099, A
43	39	43.8	401	7	US-11-096-568A-27974	Sequence 27974, A
44	39	43.8	491	7	US-11-096-568A-27973	Sequence 27973, A
45	39	43.8	542	7	US-11-087-099-8500	Sequence 8500, Ap
46	38	42.7	106	7	US-11-096-568A-14533	Sequence 14533, A
47	38	42.7	107	7	US-11-096-568A-15779	Sequence 15779, A
48	38	42.7	228	7	US-11-072-512-2829	Sequence 2829, Ap
49	38	42.7	304	6	US-10-934-944-286	Sequence 286, App
50	38	42.7	304	7	US-11-116-881A-295	Sequence 295, App
51	38	42.7	304	7	US-11-072-175-152	Sequence 152, App
52	38	42.7	518	6	US-10-934-944-298	Sequence 298, App
53	38	42.7	518	7	US-11-116-881A-307	Sequence 307, App
54	38	42.7	622	7	US-11-087-099-4176	Sequence 4176, Ap
55	38	42.7	644	7	US-11-087-099-6153	Sequence 6153, Ap
56	38	42.7	675	6	US-10-467-657-3802	Sequence 3802, Ap
57	38	42.7	851	7	US-11-087-099-2486	Sequence 2486, Ap
58	38	42.7	1215	6	US-10-964-313-6	Sequence 6, Appl
59	38	42.7	1730	7	US-11-182-016-19	Sequence 19, Appl
60	37	41.6	78	7	US-11-096-568A-4913	Sequence 4913, Ap
61	37	41.6	93	7	US-11-096-568A-4912	Sequence 4912, Ap
62	37	41.6	239	7	US-11-096-568A-14888	Sequence 14888, A
63	37	41.6	251	7	US-11-072-512-3110	Sequence 3110, Ap
64	37	41.6	251	7	US-11-096-568A-14887	Sequence 14887, A
65	37	41.6	287	7	US-11-087-099-8917	Sequence 8917, Ap
66	37	41.6	301	7	US-11-096-568A-12647	Sequence 12647, A
67	37	41.6	307	7	US-11-096-568A-25545	Sequence 25545, A
68	37	41.6	313	7	US-11-096-568A-25544	Sequence 25544, A
69	37	41.6	314	7	US-11-087-099-5913	Sequence 5913, Ap
70	37	41.6	323	6	US-10-878-556A-12	Sequence 12, Appl
71	37	41.6	323	6	US-10-878-556A-13	Sequence 13, Appl
72	37	41.6	345	7	US-11-096-568A-25543	Sequence 25543, A
73	37	41.6	364	6	US-10-623-155-172	Sequence 172, App
74	37	41.6	371	6	US-10-623-155-433	Sequence 433, App
75	37	41.6	455	7	US-11-098-686-10673	Sequence 10673, A
76	37	41.6	472	7	US-11-096-568A-12646	Sequence 12646, A
77	37	41.6	479	7	US-11-087-099-11307	Sequence 11307, A
78	37	41.6	490	7	US-11-096-568A-12645	Sequence 12645, A
79	37	41.6	498	7	US-11-087-099-3874	Sequence 3874, Ap
80	37	41.6	498	7	US-11-087-099-6654	Sequence 6654, Ap
81	37	41.6	499	7	US-11-087-099-2979	Sequence 2979, Ap
82	37	41.6	501	7	US-11-087-099-5997	Sequence 5997, Ap
83	37	41.6	501	7	US-11-087-099-8133	Sequence 8133, Ap
84	37	41.6	501	7	US-11-087-099-9295	Sequence 9295, Ap
85	37	41.6	502	7	US-11-087-099-8267	Sequence 8267, Ap
86	37	41.6	503	7	US-11-087-099-9082	Sequence 9082, Ap
87	37	41.6	504	7	US-11-087-099-2131	Sequence 2131, Ap
88	37	41.6	513	6	US-10-131-826A-536	Sequence 536, App
89	37	41.6	513	6	US-10-063-703-124	Sequence 124, App
90	37	41.6	513	6	US-10-934-944-272	Sequence 272, App
91	37	41.6	513	6	US-10-973-115B-536	Sequence 536, App
92	37	41.6	513	6	US-11-102-240-124	Sequence 124, App
93	37	41.6	513	7	US-11-116-881A-281	Sequence 281, App
94	37	41.6	513	7	US-11-103-195-124	Sequence 124, App
95	37	41.6	555	7	US-11-096-568A-24787	Sequence 24787, A
96	37	41.6	603	7	US-11-024-959-484	Sequence 484, App
97	37	41.6	704	7	US-11-096-568A-24786	Sequence 24786, A
98	37	41.6	745	7	US-11-096-568A-24785	Sequence 24785, A

99	36.5	41.0	18	6	US-10-939-890-132	Sequence 132, App	172	35	39.3	756	6	US-10-055-877-187	Sequence 187, App
100	36.5	41.0	979	6	US-10-636-320-6	Sequence 6, Appli	173	35	39.3	756	6	US-10-055-877-188	Sequence 188, App
101	36	40.4	61	6	US-10-934-944-74	Sequence 74, Appl	174	35	39.3	756	6	US-10-055-877-189	Sequence 189, App
102	36	40.4	61	6	US-11-116-881A-83	Sequence 83, Appl	175	35	39.3	830	6	US-10-055-877-190	Sequence 190, App
103	36	40.4	154	6	US-10-793-626-712	Sequence 712, App	176	35	39.3	1130	6	US-11-086-482-1	Sequence 1, Appli
104	36	40.4	159	7	US-11-071-512-2779	Sequence 2779, Ap	177	35	39.3	1130	6	US-11-192-341-23	Sequence 23, Appl
105	36	40.4	187	7	US-11-096-568A-23128	Sequence 23128, A	178	35	39.3	1367	6	US-10-995-561-538	Sequence 538, App
106	36	40.4	189	7	US-11-096-568A-23127	Sequence 23127, A	179	35	39.3	1367	6	US-10-510-903-10	Sequence 10, Appl
107	36	40.4	219	7	US-11-096-568A-18567	Sequence 18567, A	180	35	39.3	1367	6	US-11-113-202-18	Sequence 18, Appl
108	36	40.4	230	6	US-10-527-500-71	Sequence 71, Appl	181	35	39.3	1368	6	US-10-995-561-539	Sequence 539, App
109	36	40.4	251	6	US-10-527-500-3	Sequence 3, Appli	182	34.5	38.8	119	7	US-11-072-512-3261	Sequence 3261, Ap
110	36	40.4	288	7	US-11-096-568A-20363	Sequence 20363, A	183	34.5	38.8	367	7	US-11-096-568A-13389	Sequence 13389, A
111	36	40.4	291	7	US-11-096-568A-17273	Sequence 17273, A	184	34.5	38.8	388	7	US-11-096-568A-13388	Sequence 13388, A
112	36	40.4	312	7	US-11-096-568A-20362	Sequence 20362, A	185	34.5	38.8	397	7	US-11-096-568A-13387	Sequence 13387, A
113	36	40.4	331	7	US-11-087-099-9032	Sequence 9032, Ap	186	34.5	38.8	626	7	US-11-050-346-19	Sequence 19, Appl
114	36	40.4	331	7	US-11-087-099-10488	Sequence 10488, A	187	34.5	38.8	1193	7	US-11-022-478-8	Sequence 8, Appl
115	36	40.4	336	7	US-11-096-568A-15586	Sequence 15586, A	188	34.5	38.8	1218	6	US-10-501-035-303	Sequence 303, App
116	36	40.4	348	7	US-11-024-958-475	Sequence 475, App	189	34.5	38.8	1218	7	US-11-078-735-20	Sequence 20, Appl
117	36	40.4	374	7	US-11-072-175-148	Sequence 148, App	190	34.5	38.8	1218	7	US-11-050-346-65	Sequence 65, Appl
118	36	40.4	374	7	US-11-087-099-9565	Sequence 9565, Ap	191	34.5	38.8	1218	7	US-11-103-077-20	Sequence 20, Appl
119	36	40.4	386	7	US-11-096-568A-20361	Sequence 20361, A	192	34.5	38.8	1218	7	US-11-072-175-155	Sequence 155, App
120	36	40.4	429	7	US-11-087-099-8804	Sequence 8804, Ap	193	34.5	38.8	5179	7	US-11-022-478-4	Sequence 4, Appli
121	36	40.4	430	7	US-11-090-617-564	Sequence 564, App	194	34	38.2	23	6	US-10-939-890-320	Sequence 320, App
122	36	40.4	445	7	US-11-146-428-110	Sequence 110, App	195	34	38.2	23	6	US-10-939-890-444	Sequence 444, App
123	36	40.4	499	6	US-10-770-728-74	Sequence 74, Appl	196	34	38.2	23	6	US-10-939-890-709	Sequence 709, App
124	36	40.4	517	6	US-10-055-877-304	Sequence 304, App	197	34	38.2	23	6	US-10-957-351-2	Sequence 2, Appli
125	36	40.4	532	7	US-11-087-099-3353	Sequence 3353, Ap	198	34	38.2	37	6	US-11-123-896-111	Sequence 111, App
126	36	40.4	535	7	US-11-087-099-2008	Sequence 2008, Ap	199	34	38.2	56	7	US-11-123-896-114	Sequence 114, App
127	36	40.4	749	6	US-10-481-935A-105	Sequence 105, App	200	34	38.2	73	7	US-11-107-643-2	Sequence 2, Appli
128	36	40.4	984	7	US-11-182-885-2	Sequence 2, Appli	201	34	38.2	73	7	US-11-107-643-3	Sequence 3, Appli
129	36	40.4	998	7	US-11-203-251A-83	Sequence 83, Appl	202	34	38.2	75	7	US-11-004-399-2811	Sequence 2811, Ap
130	36	40.4	1182	7	US-11-182-885-6	Sequence 6, Appli	203	34	38.2	90	7	US-11-123-896-110	Sequence 110, App
131	36	40.4	1189	7	US-11-182-885-3	Sequence 3, Appli	204	34	38.2	91	7	US-11-123-896-113	Sequence 113, App
132	36	40.4	1189	7	US-11-182-885-4	Sequence 4, Appli	205	34	38.2	109	7	US-11-087-099-5318	Sequence 5318, Ap
133	36	40.4	1207	7	US-11-182-885-5	Sequence 5, Appli	206	34	38.2	120	7	US-11-072-512-2575	Sequence 2575, Ap
134	36	40.4	5405	7	US-11-108-172-1116	Sequence 1116, Ap	207	34	38.2	130	5	US-09-978-360A-690	Sequence 690, App
135	35.5	39.9	98	5	US-09-978-360A-480	Sequence 480, App	208	34	38.2	132	7	US-11-096-568A-14484	Sequence 14484, A
136	35.5	39.9	98	5	US-09-978-360A-681	Sequence 681, App	209	34	38.2	132	7	US-11-096-568A-14483	Sequence 14483, A
137	35.5	39.9	154	5	US-09-978-360A-535	Sequence 535, App	210	34	38.2	135	7	US-11-096-568A-14132	Sequence 14132, A
138	35.5	39.9	154	5	US-09-978-360A-627	Sequence 627, App	211	34	38.2	139	7	US-11-096-568A-14132	Sequence 14132, A
139	35.5	39.9	183	5	US-09-978-360A-680	Sequence 680, App	212	34	38.2	152	7	US-11-096-568A-13839	Sequence 13839, A
140	35.5	39.9	454	7	US-11-072-512-2092	Sequence 2092, Ap	213	34	38.2	153	7	US-11-096-568A-13838	Sequence 13838, A
141	35	39.3	17	7	US-11-152-974A-153	Sequence 153, App	214	34	38.2	162	7	US-11-096-568A-24083	Sequence 24083, A
142	35	39.3	17	7	US-11-153-143A-153	Sequence 153, App	215	34	38.2	189	7	US-11-096-568A-13837	Sequence 13837, A
143	35	39.3	30	7	US-11-120-501-29	Sequence 29, Appl	216	34	38.2	211	7	US-11-096-568A-7	Sequence 7, Appli
144	35	39.3	46	7	US-11-240-769-123	Sequence 123, App	217	34	38.2	213	7	US-11-183-555-6	Sequence 6, Appli
145	35	39.3	68	6	US-10-892-379-12	Sequence 12, Appl	218	34	38.2	213	7	US-11-107-643-1	Sequence 1, Appli
146	35	39.3	79	7	US-11-087-099-11235	Sequence 11235, A	219	34	38.2	217	7	US-11-096-568A-6	Sequence 6, Appli
147	35	39.3	98	7	US-11-086-482-6	Sequence 6, Appli	220	34	38.2	223	7	US-11-096-568A-5	Sequence 5, Appli
148	35	39.3	129	7	US-11-072-512-2426	Sequence 2426, Ap	221	34	38.2	225	7	US-11-183-089-2	Sequence 2, Appli
149	35	39.3	136	7	US-11-096-568A-4627	Sequence 4627, Ap	222	34	38.2	234	7	US-11-096-568A-32205	Sequence 32205, A
150	35	39.3	137	7	US-11-096-568A-4626	Sequence 4626, Ap	223	34	38.2	235	6	US-10-821-234-1398	Sequence 1398, Ap
151	35	39.3	143	7	US-11-240-769-122	Sequence 122, App	224	34	38.2	240	7	US-11-096-568A-32204	Sequence 32204, A
152	35	39.3	148	7	US-11-096-568A-4625	Sequence 4625, Ap	225	34	38.2	246	7	US-11-096-568A-32203	Sequence 32203, A
153	35	39.3	157	6	US-10-475-075-785	Sequence 785, App	226	34	38.2	252	6	US-10-527-500-19	Sequence 19, Appl
154	35	39.3	273	7	US-11-086-482-4	Sequence 4, Appli	227	34	38.2	252	7	US-11-096-568A-2866	Sequence 2866, Ap
155	35	39.3	273	7	US-11-087-099-11703	Sequence 1703, Ap	228	34	38.2	255	6	US-10-454-437-150	Sequence 150, App
156	35	39.3	293	7	US-11-092-168-11	Sequence 11, Appl	229	34	38.2	259	7	US-10-454-437-152	Sequence 49, Appl
157	35	39.3	310	7	US-11-086-482-3	Sequence 3, Appli	230	34	38.2	259	7	US-11-052-554A-49	Sequence 199, App
158	35	39.3	330	7	US-11-206-587-8	Sequence 8, Appli	231	34	38.2	261	6	US-10-511-758-1	Sequence 76, Appl
159	35	39.3	343	7	US-11-096-568A-5698	Sequence 5698, Ap	232	34	38.2	261	6	US-10-511-758-1	Sequence 1, Appli
160	35	39.3	361	7	US-11-096-568A-5697	Sequence 5697, Ap	233	34	38.2	261	7	US-11-096-568A-5767	Sequence 5767, Ap
161	35	39.3	362	7	US-11-096-568A-5696	Sequence 5696, Ap	234	34	38.2	263	7	US-11-096-568A-5766	Sequence 5766, Ap
162	35	39.3	421	7	US-11-087-099-11711	Sequence 11711, A	235	34	38.2	267	7	US-11-096-568A-17567	Sequence 17567, A
163	35	39.3	422	6	US-10-632-150-4	Sequence 4, Appli	236	34	38.2	283	7	US-11-096-568A-33129	Sequence 33129, A
164	35	39.3	422	7	US-11-073-457-4	Sequence 4, Appli	237	34	38.2	283	7	US-11-096-568A-33128	Sequence 33128, A
165	35	39.3	422	7	US-11-073-460-4	Sequence 4, Appli	238	34	38.2	295	7	US-11-096-568A-33128	Sequence 2432, Ap
166	35	39.3	524	6	US-10-995-561-789	Sequence 789, App	239	34	38.2	306	7	US-11-172-740-2432	Sequence 29443, A
167	35	39.3	547	6	US-10-995-561-785	Sequence 785, App	240	34	38.2	314	7	US-11-096-568A-29443	Sequence 29443, A
168	35	39.3	547	6	US-10-995-561-787	Sequence 787, App	241	34	38.2	323	6	US-10-511-758-16	Sequence 16, Appl
169	35	39.3	547	6	US-10-493-909-65	Sequence 65, Appl	242	34	38.2	324	7	US-11-096-568A-29442	Sequence 29442, A
170	35	39.3	547	7	US-11-107-028-24	Sequence 24, Appl	243	34	38.2	329	7	US-11-096-568A-29441	Sequence 29441, A
171	35	39.3	756	6	US-10-055-877-34	Sequence 34, Appl	244	34	38.2	362	7	US-11-109-157A-8	Sequence 8, Appli

245	34	38.2	370	7	US-11-109-157A-41	Sequence 41, Appl	318	33.5	37.6	585	7	US-11-108-172-1067	Sequence 1067, Ap
246	34	38.2	377	7	US-11-240-769-67	Sequence 67, Appl	319	33	37.1	11	7	US-11-004-399-1178	Sequence 1178, Ap
247	34	38.2	377	7	US-11-096-568A-2865	Sequence 2865, Ap	320	33	37.1	16	7	US-11-198-847-309	Sequence 309, App
248	34	38.2	377	7	US-11-096-568A-2867	Sequence 2867, Ap	321	33	37.1	17	7	US-11-152-974A-201	Sequence 201, App
249	34	38.2	378	7	US-11-087-099-1091	Sequence 1091, Ap	322	33	37.1	17	7	US-11-153-143A-201	Sequence 201, App
250	34	38.2	382	7	US-11-087-099-3195	Sequence 3195, Ap	323	33	37.1	40	7	US-11-096-568A-2049	Sequence 2049, Ap
251	34	38.2	394	7	US-11-096-568A-5765	Sequence 5765, Ap	324	33	37.1	86	7	US-11-096-568A-2263	Sequence 2263, Ap
252	34	38.2	396	7	US-11-096-568A-33127	Sequence 33127, A	325	33	37.1	92	7	US-11-096-568A-2262	Sequence 2262, Ap
253	34	38.2	398	7	US-11-072-512-2769	Sequence 2769, Ap	326	33	37.1	95	6	US-10-995-561-620	Sequence 620, App
254	34	38.2	409	7	US-11-096-568A-32946	Sequence 32946, A	327	33	37.1	102	7	US-11-072-512-2266	Sequence 2266, Ap
255	34	38.2	431	7	US-11-096-568A-7306	Sequence 7306, Ap	328	33	37.1	107	6	US-10-517-636-119	Sequence 119, App
256	34	38.2	448	7	US-11-096-568A-22630	Sequence 22630, A	329	33	37.1	108	7	US-11-087-099-5377	Sequence 5377, Ap
257	34	38.2	450	7	US-11-096-568A-22629	Sequence 22629, A	330	33	37.1	111	7	US-11-072-512-2282	Sequence 2282, Ap
258	34	38.2	456	7	US-11-096-568A-32945	Sequence 32945, A	331	33	37.1	118	7	US-11-072-512-3051	Sequence 3051, Ap
259	34	38.2	457	6	US-10-951-236-1	Sequence 1, Appli	332	33	37.1	121	7	US-11-087-099-2574	Sequence 2574, Ap
260	34	38.2	457	6	US-10-951-236-10	Sequence 10, Appl	333	33	37.1	127	7	US-11-096-568A-17924	Sequence 17924, A
261	34	38.2	463	7	US-11-096-568A-1881	Sequence 1881, Ap	334	33	37.1	132	7	US-11-169-041-187	Sequence 187, App
262	34	38.2	474	7	US-11-087-099-10357	Sequence 10357, A	335	33	37.1	150	7	US-11-096-568A-24935	Sequence 24935, A
263	34	38.2	475	7	US-11-174-150-45	Sequence 45, Appl	336	33	37.1	153	7	US-11-096-568A-5443	Sequence 5443, Ap
264	34	38.2	487	7	US-11-096-568A-1880	Sequence 1880, Ap	337	33	37.1	161	7	US-11-087-099-4335	Sequence 4335, Ap
265	34	38.2	491	7	US-11-087-099-252	Sequence 252, App	338	33	37.1	162	7	US-11-096-568A-14218	Sequence 14218, A
266	34	38.2	491	7	US-11-087-099-10555	Sequence 10555, A	339	33	37.1	164	7	US-11-096-568A-12820	Sequence 12820, A
267	34	38.2	493	7	US-11-087-099-9453	Sequence 9453, Ap	340	33	37.1	175	7	US-11-096-568A-6628	Sequence 6628, Ap
268	34	38.2	499	7	US-11-087-099-5135	Sequence 5135, Ap	341	33	37.1	183	7	US-11-096-568A-17923	Sequence 17923, A
269	34	38.2	499	7	US-11-087-099-10929	Sequence 10929, A	342	33	37.1	199	7	US-11-096-568A-17922	Sequence 17922, A
270	34	38.2	500	7	US-11-096-568A-2864	Sequence 2864, Ap	343	33	37.1	202	7	US-11-096-568A-25790	Sequence 25790, A
271	34	38.2	502	7	US-11-096-568A-1879	Sequence 1879, Ap	344	33	37.1	252	6	US-10-055-877-107	Sequence 107, App
272	34	38.2	503	7	US-11-087-099-6570	Sequence 6570, Ap	345	33	37.1	252	7	US-11-072-512-2305	Sequence 2305, Ap
273	34	38.2	504	7	US-11-087-099-2620	Sequence 2620, Ap	346	33	37.1	255	7	US-11-087-099-8356	Sequence 8356, Ap
274	34	38.2	512	7	US-11-172-740-2433	Sequence 2433, Ap	347	33	37.1	255	7	US-11-087-099-11594	Sequence 11594, A
275	34	38.2	517	6	US-10-934-944-230	Sequence 230, App	348	33	37.1	276	6	US-10-055-877-111	Sequence 111, App
276	34	38.2	517	6	US-11-116-881A-239	Sequence 239, App	349	33	37.1	276	6	US-10-055-877-115	Sequence 115, App
277	34	38.2	522	6	US-10-995-561-1030	Sequence 1030, Ap	350	33	37.1	309	7	US-11-087-099-10426	Sequence 10426, A
278	34	38.2	523	7	US-11-096-568A-5649	Sequence 5649, Ap	351	33	37.1	315	7	US-11-096-568A-6627	Sequence 6627, Ap
279	34	38.2	523	7	US-11-172-740-2435	Sequence 2435, Ap	352	33	37.1	323	7	US-11-096-568A-6626	Sequence 6626, Ap
280	34	38.2	524	7	US-11-096-568A-5648	Sequence 5648, Ap	353	33	37.1	333	7	US-11-087-099-2504	Sequence 2504, Ap
281	34	38.2	529	7	US-11-174-150-46	Sequence 46, Appl	354	33	37.1	344	6	US-10-537-075-19	Sequence 19, Appl
282	34	38.2	534	6	US-10-793-626-920	Sequence 920, App	355	33	37.1	345	7	US-11-087-099-8454	Sequence 8454, Ap
283	34	38.2	540	6	US-10-485-517-223	Sequence 223, App	356	33	37.1	348	6	US-10-512-277-1	Sequence 1, Appli
284	34	38.2	554	6	US-10-850-816-6	Sequence 6, Appli	357	33	37.1	351	7	US-11-087-099-7115	Sequence 7115, Ap
285	34	38.2	560	6	US-10-995-561-1026	Sequence 1026, Ap	358	33	37.1	389	7	US-11-096-568A-21738	Sequence 21738, A
286	34	38.2	597	7	US-11-087-099-11607	Sequence 11607, A	359	33	37.1	392	7	US-11-096-568A-21737	Sequence 21737, A
287	34	38.2	597	7	US-11-124-367A-389	Sequence 389, App	360	33	37.1	393	7	US-11-096-568A-29771	Sequence 29771, A
288	34	38.2	599	7	US-11-124-367A-390	Sequence 390, App	361	33	37.1	394	7	US-11-087-099-11230	Sequence 11230, A
289	34	38.2	599	7	US-11-124-367A-391	Sequence 391, App	362	33	37.1	419	7	US-11-096-568A-29053	Sequence 29053, A
290	34	38.2	599	7	US-11-124-367A-392	Sequence 392, App	363	33	37.1	420	7	US-11-096-568A-21736	Sequence 21736, A
291	34	38.2	616	6	US-10-995-561-1018	Sequence 1018, Ap	364	33	37.1	421	7	US-11-087-099-4040	Sequence 4040, Ap
292	34	38.2	616	6	US-10-995-561-1022	Sequence 1022, Ap	365	33	37.1	424	7	US-11-096-568A-17960	Sequence 17960, A
293	34	38.2	618	7	US-11-087-099-5707	Sequence 5707, Ap	366	33	37.1	429	7	US-11-096-568A-17959	Sequence 17959, A
294	34	38.2	618	7	US-11-087-099-7200	Sequence 7200, Ap	367	33	37.1	430	7	US-11-096-568A-17958	Sequence 17958, A
295	34	38.2	649	7	US-11-109-157A-7	Sequence 7, Appli	368	33	37.1	431	7	US-11-096-568A-29052	Sequence 29052, A
296	34	38.2	716	7	US-11-096-568A-29226	Sequence 29226, A	369	33	37.1	443	7	US-11-096-568A-18212	Sequence 18212, A
297	34	38.2	722	7	US-11-096-568A-29225	Sequence 29225, A	370	33	37.1	445	7	US-11-096-568A-2542	Sequence 2542, Ap
298	34	38.2	732	6	US-10-518-599-23	Sequence 23, Appl	371	33	37.1	452	7	US-11-096-568A-24185	Sequence 24185, A
299	34	38.2	732	6	US-10-995-561-1020	Sequence 1020, Ap	372	33	37.1	452	7	US-11-096-568A-34038	Sequence 34038, A
300	34	38.2	737	6	US-11-096-568A-29224	Sequence 29224, A	373	33	37.1	457	7	US-11-096-568A-5002	Sequence 5002, Ap
301	34	38.2	757	6	US-10-055-877-190	Sequence 190, App	374	33	37.1	458	7	US-11-096-568A-5001	Sequence 5001, Ap
302	34	38.2	774	6	US-10-055-877-191	Sequence 191, App	375	33	37.1	464	6	US-10-453-372-1138	Sequence 1138, Ap
303	34	38.2	785	7	US-11-109-157A-6	Sequence 6, Appli	376	33	37.1	467	6	US-10-453-372-1140	Sequence 1140, Ap
304	34	38.2	1076	7	US-11-109-157A-5	Sequence 5, Appli	377	33	37.1	485	7	US-11-087-099-3751	Sequence 9751, Ap
305	34	38.2	1160	6	US-10-995-561-1019	Sequence 1019, Ap	378	33	37.1	495	7	US-11-087-099-3101	Sequence 3101, Ap
306	34	38.2	1302	6	US-10-995-561-1024	Sequence 1024, Ap	379	33	37.1	498	7	US-11-096-568A-24184	Sequence 24184, A
307	34	38.2	1306	6	US-10-995-561-1027	Sequence 1027, Ap	380	33	37.1	501	6	US-10-630-203-27	Sequence 27, Appl
308	34	38.2	1907	7	US-11-039-398-25	Sequence 25, Appl	381	33	37.1	501	6	US-10-630-203-28	Sequence 28, Appl
309	33.5	37.6	141	7	US-11-072-175-202	Sequence 202, App	382	33	37.1	501	7	US-11-096-568A-5000	Sequence 5000, Ap
310	33.5	37.6	141	7	US-11-072-175-229	Sequence 229, App	383	33	37.1	504	7	US-11-096-568A-18211	Sequence 18211, A
311	33.5	37.6	152	7	US-11-096-568A-15236	Sequence 15236, A	384	33	37.1	513	6	US-10-650-326B-16	Sequence 16, Appl
312	33.5	37.6	294	7	US-11-096-568A-15235	Sequence 15235, A	385	33	37.1	513	6	US-10-921-793-16	Sequence 16, Appl
313	33.5	37.6	303	7	US-11-096-568A-15234	Sequence 15234, A	386	33	37.1	513	6	US-10-931-198-16	Sequence 16, Appl
314	33.5	37.6	352	7	US-11-087-099-10912	Sequence 10912, A	387	33	37.1	513	6	US-10-942-042-16	Sequence 16, Appl
315	33.5	37.6	381	6	US-10-517-939-326	Sequence 326, App	388	33	37.1	513	7	US-11-000-463-816	Sequence 816, App
316	33.5	37.6	413	5	US-09-978-360A-710	Sequence 710, App	389	33	37.1	522	7	US-11-087-099-6999	Sequence 6999, Ap
317	33.5	37.6	488	7	US-11-169-041-197	Sequence 197, App	390	33	37.1	523	7	US-11-024-959-371	Sequence 371, App

391	33	37.1	528	6	US-10-864-758-7	Sequence 7, Appli	464	32	36.0	395	7	US-11-087-099-5231	Sequence 5231, Ap
392	33	37.1	540	7	US-11-096-568A-18210	Sequence 18210, A	465	32	36.0	397	7	US-11-096-568A-29851	Sequence 29851, A
393	33	37.1	546	7	US-11-096-568A-24183	Sequence 24183, A	466	32	36.0	404	7	US-11-096-568A-13568	Sequence 13568, A
394	33	37.1	564	7	US-11-096-568A-2541	Sequence 2541, Ap	467	32	36.0	406	7	US-11-098-686-10564	Sequence 10564, A
395	33	37.1	602	7	US-11-096-568A-2540	Sequence 2540, Ap	468	32	36.0	417	7	US-11-186-284-107	Sequence 107, App
396	33	37.1	634	7	US-11-072-512-2300	Sequence 2300, Ap	469	32	36.0	417	7	US-11-043-806-385	Sequence 385, App
397	33	37.1	684	6	US-11-055-877-105	Sequence 105, App	470	32	36.0	419	7	US-11-096-568A-11271	Sequence 11271, A
398	33	37.1	686	7	US-11-087-099-11436	Sequence 11436, A	471	32	36.0	419	7	US-11-096-568A-29850	Sequence 29850, A
399	33	37.1	704	6	US-10-055-877-113	Sequence 113, App	472	32	36.0	420	7	US-11-096-568A-17525	Sequence 17525, A
400	33	37.1	742	7	US-11-087-099-4561	Sequence 4561, Ap	473	32	36.0	424	7	US-11-087-099-357	Sequence 357, App
401	33	37.1	743	6	US-10-055-877-109	Sequence 109, App	474	32	36.0	424	7	US-11-087-099-5191	Sequence 5191, Ap
402	33	37.1	763	7	US-11-144-985-6	Sequence 6, Appli	475	32	36.0	429	6	US-10-131-826A-94	Sequence 94, Appl
403	33	37.1	782	7	US-11-087-099-11013	Sequence 11013, A	476	32	36.0	429	6	US-10-973-115B-94	Sequence 94, Appl
404	33	37.1	783	7	US-11-192-219-7	Sequence 7, Appli	477	32	36.0	444	7	US-11-072-512-2690	Sequence 2690, Ap
405	33	37.1	867	6	US-10-725-475-19	Sequence 19, Appl	478	32	36.0	446	7	US-11-096-568A-13567	Sequence 13567, A
406	33	37.1	894	7	US-11-202-330-2	Sequence 22, Appl	479	32	36.0	447	7	US-11-112-882-4	Sequence 4, Appli
407	33	37.1	1154	6	US-10-511-989-22	Sequence 22, Appl	480	32	36.0	448	7	US-11-096-568A-24375	Sequence 24375, A
408	33	37.1	1162	7	US-11-203-330-43	Sequence 43, Appl	481	32	36.0	450	6	US-11-122-396-9	Sequence 9, Appli
409	33	37.1	1184	6	US-10-131-826A-394	Sequence 394, App	482	32	36.0	456	6	US-10-641-678-51	Sequence 51, Appl
410	33	37.1	1184	6	US-10-973-115B-394	Sequence 394, App	483	32	36.0	479	6	US-10-511-989-162	Sequence 162, App
411	33	37.1	1487	6	US-10-511-989-24	Sequence 24, Appl	484	32	36.0	497	7	US-11-087-099-5884	Sequence 5884, Ap
412	33	37.1	1866	6	US-10-511-989-186	Sequence 186, App	485	32	36.0	501	6	US-10-630-203-25	Sequence 25, Appl
413	32.5	36.5	20	7	US-11-106-415-182	Sequence 182, App	486	32	36.0	509	6	US-10-131-826A-108	Sequence 108, App
414	32.5	36.5	73	7	US-11-096-568A-17429	Sequence 17429, A	487	32	36.0	509	6	US-10-973-115B-108	Sequence 108, App
415	32.5	36.5	140	7	US-11-096-568A-1538	Sequence 1538, Ap	488	32	36.0	519	7	US-11-033-039-442	Sequence 442, App
416	32.5	36.5	353	7	US-11-017-058-9	Sequence 9, Appli	489	32	36.0	528	6	US-10-493-909-83	Sequence 83, Appl
417	32.5	36.5	355	7	US-11-218-281-26	Sequence 26, Appl	490	32	36.0	536	6	US-10-641-678-61	Sequence 61, Appl
418	32.5	36.5	383	7	US-11-147-047-38	Sequence 38, Appl	491	32	36.0	540	6	US-10-641-678-60	Sequence 60, Appl
419	32.5	36.5	420	7	US-11-230-180-18	Sequence 18, Appl	492	32	36.0	545	6	US-10-714-995-8	Sequence 8, Appli
420	32	36.0	18	7	US-11-156-163-6	Sequence 6, Appli	493	32	36.0	549	7	US-11-085-185-2	Sequence 2, Appli
421	32	36.0	59	7	US-11-096-568A-90	Sequence 90, Appl	494	32	36.0	585	7	US-11-054-281-92	Sequence 92, Appl
422	32	36.0	84	7	US-11-096-568A-8721	Sequence 8721, Ap	495	32	36.0	609	6	US-10-517-939-310	Sequence 310, App
423	32	36.0	90	7	US-11-096-568A-8720	Sequence 8720, Ap	496	32	36.0	661	7	US-11-087-099-1594	Sequence 1594, Ap
424	32	36.0	91	7	US-11-082-389-352	Sequence 352, App	497	32	36.0	673	7	US-11-072-512-2774	Sequence 2774, Ap
425	32	36.0	100	6	US-10-793-626-848	Sequence 848, App	498	32	36.0	674	6	US-10-055-877-319	Sequence 319, App
426	32	36.0	111	7	US-11-072-512-3346	Sequence 3346, Ap	499	32	36.0	687	7	US-11-117-169-6	Sequence 6, Appli
427	32	36.0	117	7	US-11-096-568A-13323	Sequence 13323, A	500	32	36.0	687	7	US-11-185-342-16	Sequence 16, Appl
428	32	36.0	118	7	US-11-240-769-66	Sequence 66, Appl	501	32	36.0	687	7	US-11-185-342-16	Sequence 16, Appl
429	32	36.0	126	7	US-11-116-939-4	Sequence 4, Appli	502	32	36.0	710	7	US-11-089-551A-33	Sequence 33, Appl
430	32	36.0	128	6	US-10-821-234-1538	Sequence 1538, Ap	503	32	36.0	717	6	US-10-624-932-12	Sequence 12, Appl
431	32	36.0	134	7	US-11-096-568A-10284	Sequence 10284, A	504	32	36.0	717	6	US-10-511-989-32	Sequence 32, Appl
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433	32	36.0	148	6	US-10-491-468-39	Sequence 39, Appl	506	32	36.0	732	6	US-10-518-599-22	Sequence 22, Appl
434	32	36.0	151	6	US-10-454-437-274	Sequence 274, App	507	32	36.0	755	7	US-11-072-512-2505	Sequence 2505, Ap
435	32	36.0	164	7	US-11-072-512-3369	Sequence 3369, Ap	508	32	36.0	760	6	US-10-821-234-1141	Sequence 1141, Ap
436	32	36.0	175	7	US-11-096-568A-2290	Sequence 2290, Ap	509	32	36.0	822	7	US-11-087-099-8165	Sequence 8165, Ap
437	32	36.0	205	7	US-11-072-512-3758	Sequence 3758, Ap	510	32	36.0	830	6	US-10-330-773-406	Sequence 406, App
438	32	36.0	206	6	US-10-055-877-192	Sequence 192, App	511	32	36.0	830	6	US-10-330-773-406	Sequence 406, App
439	32	36.0	225	7	US-11-096-568A-19289	Sequence 19289, A	512	32	36.0	834	6	US-10-501-035-280	Sequence 280, App
440	32	36.0	246	7	US-11-156-516-40	Sequence 40, Appl	513	32	36.0	851	6	US-10-330-773-397	Sequence 397, App
441	32	36.0	249	7	US-11-096-568A-19261	Sequence 19261, A	514	32	36.0	879	6	US-10-877-346-17	Sequence 17, Appl
442	32	36.0	274	7	US-11-096-568A-17297	Sequence 17297, A	515	32	36.0	879	6	US-10-877-346-52	Sequence 52, Appl
443	32	36.0	279	7	US-11-072-512-3382	Sequence 3382, Ap	516	32	36.0	879	6	US-10-877-346-53	Sequence 53, Appl
444	32	36.0	291	7	US-11-096-568A-17527	Sequence 17527, A	517	32	36.0	879	6	US-10-877-346-54	Sequence 54, Appl
445	32	36.0	316	7	US-11-197-133A-6	Sequence 6, Appli	518	32	36.0	896	6	US-10-467-657-7004	Sequence 7004, Ap
446	32	36.0	316	7	US-11-096-568A-10754	Sequence 10754, A	519	32	36.0	896	7	US-11-192-219-3	Sequence 3, Appli
447	32	36.0	330	6	US-10-332-186-1	Sequence 1, Appli	520	32	36.0	898	7	US-11-166-720-3	Sequence 3, Appli
448	32	36.0	336	7	US-11-087-099-9106	Sequence 9106, Ap	521	32	36.0	923	7	US-11-192-219-4	Sequence 4, Appli
449	32	36.0	340	7	US-11-087-099-1074	Sequence 1074, Ap	522	32	36.0	940	6	US-10-511-989-34	Sequence 34, Appl
450	32	36.0	345	7	US-11-096-568A-17526	Sequence 17526, A	523	32	36.0	970	7	US-11-037-243-101	Sequence 101, App
451	32	36.0	347	7	US-11-186-284-236	Sequence 236, App	524	32	36.0	977	6	US-10-511-989-149	Sequence 149, App
452	32	36.0	349	7	US-11-096-568A-13569	Sequence 13569, A	525	32	36.0	1101	6	US-10-878-556A-107	Sequence 107, App
453	32	36.0	350	7	US-11-096-568A-16922	Sequence 16922, A	526	32	36.0	1164	7	US-11-087-099-2278	Sequence 2278, Ap
454	32	36.0	358	7	US-11-096-568A-16921	Sequence 16921, A	527	32	36.0	1164	7	US-11-087-099-9070	Sequence 9070, Ap
455	32	36.0	359	7	US-11-096-568A-11100	Sequence 11100, A	528	32	36.0	1165	7	US-11-192-219-2	Sequence 2, Appli
456	32	36.0	362	7	US-11-096-568A-16920	Sequence 16920, A	529	32	36.0	1165	6	US-10-613-744-9	Sequence 9, Appli
457	32	36.0	367	7	US-11-087-099-8709	Sequence 8709, Ap	530	32	36.0	1196	6	US-11-152-974A-254	Sequence 254, App
458	32	36.0	368	7	US-11-087-099-4066	Sequence 4066, Ap	531	31.5	35.4	16	7	US-11-153-143A-254	Sequence 254, App
459	32	36.0	375	7	US-11-087-099-8271	Sequence 8271, Ap	532	31.5	35.4	16	7	US-11-153-143A-254	Sequence 254, App
460	32	36.0	376	7	US-11-024-954-434	Sequence 434, App	533	31.5	35.4	167	7	US-11-172-740-1275	Sequence 1275, Ap
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462	32	36.0	387	7	US-11-096-568A-11098	Sequence 11098, A	535	31.5	35.4	167	7	US-11-236-198-34	Sequence 34, Appl
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539	31.5	35.4	243	6	US-10-512-109-23	Sequence 23, Appl	612	31	34.8	262	7	US-11-009-658-2	Sequence 2, Appli
540	31.5	35.4	243	6	US-10-512-109-48	Sequence 48, Appl	613	31	34.8	272	6	US-10-793-628-588	Sequence 588, App
541	31.5	35.4	268	6	US-10-467-657-7312	Sequence 7312, Ap	614	31	34.8	276	7	US-11-062-186-40	Sequence 40, Appl
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543	31.5	35.4	397	7	US-11-192-219-47	Sequence 47, Appl	616	31	34.8	277	7	US-11-182-946-10	Sequence 10, Appl
544	31.5	35.4	424	7	US-11-185-230-6	Sequence 6, Appli	617	31	34.8	277	7	US-11-033-039-858	Sequence 858, App
545	31.5	35.4	424	7	US-11-182-384A-6	Sequence 6, Appli	618	31	34.8	277	7	US-11-127-046-2	Sequence 2, Appli
546	31.5	35.4	424	7	US-11-182-384A-6	Sequence 6, Appli	619	31	34.8	277	7	US-11-169-041-196	Sequence 196, App
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559	31	34.8	16	7	US-11-152-974A-255	Sequence 255, App	632	31	34.8	327	7	US-11-096-568A-6294	Sequence 6294, Ap
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561	31	34.8	16	7	US-11-153-143A-255	Sequence 255, App	634	31	34.8	335	6	US-10-995-561-866	Sequence 10, Appl
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563	31	34.8	19	6	US-10-939-890-221	Sequence 221, App	636	31	34.8	336	7	US-11-099-691-8	Sequence 2029, Ap
564	31	34.8	20	7	US-11-004-399-2217	Sequence 2217, Ap	637	31	34.8	339	7	US-11-072-512-2029	Sequence 2, Appli
565	31	34.8	21	6	US-10-939-890-515	Sequence 515, App	638	31	34.8	339	7	US-11-010-874-2	Sequence 32, Appl
566	31	34.8	28	7	US-11-121-044A-97	Sequence 34, Appl	639	31	34.8	344	7	US-11-108-163B-10	Sequence 10, Appl
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568	31	34.8	34	7	US-11-004-399-203	Sequence 203, App	641	31	34.8	349	7	US-11-024-959-464	Sequence 464, App
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571	31	34.8	49	7	US-11-123-896-78	Sequence 78, Appl	644	31	34.8	360	7	US-11-087-099-9828	Sequence 9828, Ap
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575	31	34.8	61	7	US-11-116-881A-81	Sequence 81, Appl	648	31	34.8	361	7	US-11-087-099-9826	Sequence 9826, Ap
576	31	34.8	61	7	US-11-116-881A-85	Sequence 85, Appl	649	31	34.8	361	7	US-11-087-099-11472	Sequence 11472, A
577	31	34.8	62	7	US-11-000-463-933	Sequence 933, App	650	31	34.8	362	7	US-11-087-099-9055	Sequence 9055, App
578	31	34.8	68	6	US-10-467-657-1436	Sequence 1436, Ap	651	31	34.8	368	7	US-11-087-099-9366	Sequence 936, App
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581	31	34.8	81	6	US-10-467-657-5668	Sequence 5668, Ap	654	31	34.8	371	7	US-11-009-658-28	Sequence 28, Appl
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583	31	34.8	81	6	US-10-467-657-8352	Sequence 8352, Ap	656	31	34.8	372	6	US-10-995-561-948	Sequence 948, App
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586	31	34.8	98	7	US-11-096-568A-29	Sequence 29, Appl	659	31	34.8	374	6	US-10-995-561-946	Sequence 946, App
587	31	34.8	123	7	US-11-072-512-3670	Sequence 3670, Ap	660	31	34.8	385	6	US-10-995-561-945	Sequence 945, App
588	31	34.8	123	7	US-11-072-512-3934	Sequence 3934, Ap	661	31	34.8	385	6	US-10-995-561-949	Sequence 949, App
589	31	34.8	146	6	US-10-467-657-5594	Sequence 5594, Ap	662	31	34.8	390	6	US-10-467-657-3212	Sequence 3212, Ap
590	31	34.8	153	7	US-11-096-568A-12020	Sequence 12020, A	663	31	34.8	391	6	US-11-105-172-4	Sequence 4, Appli
591	31	34.8	156	7	US-11-072-512-2055	Sequence 2055, A	664	31	34.8	393	7	US-11-087-099-1949	Sequence 1949, Ap
592	31	34.8	157	7	US-11-096-568A-14398	Sequence 14398, A	665	31	34.8	394	6	US-10-392-234A-46	Sequence 46, Appl
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595	31	34.8	168	7	US-11-010-874-7	Sequence 7, Appli	668	31	34.8	398	6	US-10-498-026-93	Sequence 93, Appl
596	31	34.8	172	7	US-11-096-568A-16967	Sequence 16967, A	669	31	34.8	411	6	US-10-524-919-4	Sequence 4, Appli
597	31	34.8	178	7	US-11-087-099-3667	Sequence 3667, Ap	670	31	34.8	412	6	US-10-524-919-2	Sequence 2, Appli
598	31	34.8	191	6	US-10-924-074-4	Sequence 4, Appli	671	31	34.8	417	7	US-11-174-467-10	Sequence 10, Appl
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603	31	34.8	217	6	US-10-793-626-1968	Sequence 1968, Ap	676	31	34.8	442	7	US-11-172-740-459	Sequence 459, App
604	31	34.8	225	7	US-11-096-568A-18284	Sequence 18284, A	677	31	34.8	442	7	US-11-172-740-706	Sequence 706, App
605	31	34.8	229	6	US-10-924-074-8	Sequence 8, Appli	678	31	34.8	443	7	US-11-087-099-10930	Sequence 10930, A
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607	31	34.8	241	7	US-11-096-568A-6296	Sequence 6296, Ap	680	31	34.8	444	7	US-11-172-740-461	Sequence 461, App
608	31	34.8	244	6	US-10-924-074-2	Sequence 2, Appli	681	31	34.8	444	7	US-11-172-740-716	Sequence 716, App
609	31	34.8	251	7	US-11-096-568A-18283	Sequence 18283, A	682	31	34.8	444	7		

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684	31	34.8	445	7	US-11-172-740-460	Sequence 460, App	757	31	34.8	607	7	US-11-143-984A-150	Sequence 150, App
685	31	34.8	445	7	US-11-172-740-462	Sequence 462, App	758	31	34.8	625	6	US-10-501-035-381	Sequence 381, App
686	31	34.8	445	7	US-11-172-740-465	Sequence 465, App	759	31	34.8	628	7	US-11-024-959-416	Sequence 416, App
687	31	34.8	445	7	US-11-172-740-467	Sequence 467, App	760	31	34.8	629	7	US-11-087-099-6338	Sequence 6338, App
688	31	34.8	445	7	US-11-172-740-708	Sequence 708, App	761	31	34.8	662	7	US-11-143-984A-178	Sequence 178, App
689	31	34.8	445	7	US-11-172-740-711	Sequence 711, App	762	31	34.8	699	7	US-11-143-984A-177	Sequence 177, App
690	31	34.8	445	7	US-11-172-740-714	Sequence 714, App	763	31	34.8	716	6	US-10-467-657-6200	Sequence 6200, App
691	31	34.8	445	7	US-11-172-740-715	Sequence 715, App	764	31	34.8	744	6	US-10-467-657-1936	Sequence 1936, App
692	31	34.8	447	7	US-11-172-740-466	Sequence 466, App	765	31	34.8	747	7	US-11-143-984A-176	Sequence 176, App
693	31	34.8	447	7	US-11-172-740-468	Sequence 468, App	766	31	34.8	776	7	US-11-096-568A-28301	Sequence 28301, A
694	31	34.8	447	7	US-11-172-740-713	Sequence 713, App	767	31	34.8	778	6	US-10-330-773-846	Sequence 846, App
695	31	34.8	448	7	US-11-096-568A-24243	Sequence 24243, A	768	31	34.8	806	7	US-11-143-984A-175	Sequence 175, App
696	31	34.8	453	7	US-11-087-099-3550	Sequence 3550, App	769	31	34.8	808	7	US-11-110-082-38	Sequence 38, Appl
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698	31	34.8	456	7	US-11-000-463-923	Sequence 923, App	771	31	34.8	812	7	US-11-108-459-6	Sequence 5, Appli
699	31	34.8	456	7	US-11-024-959-480	Sequence 480, App	772	31	34.8	833	7	US-11-076-187-5	Sequence 327, App
700	31	34.8	461	7	US-11-024-959-507	Sequence 507, App	773	31	34.8	847	6	US-10-501-035-327	Sequence 327, App
701	31	34.8	463	7	US-11-096-568A-14680	Sequence 14680, A	774	31	34.8	860	7	US-11-022-562-217	Sequence 217, App
702	31	34.8	467	7	US-11-000-463-452	Sequence 452, App	775	31	34.8	863	6	US-10-330-773-849	Sequence 849, App
703	31	34.8	467	7	US-11-000-463-924	Sequence 924, App	776	31	34.8	897	7	US-11-087-099-706	Sequence 706, App
704	31	34.8	467	7	US-11-000-463-925	Sequence 925, App	777	31	34.8	954	6	US-10-467-657-31	Sequence 31, Appl
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706	31	34.8	470	7	US-11-024-959-297	Sequence 297, App	779	31	34.8	1083	7	US-11-113-751-40	Sequence 40, Appl
707	31	34.8	470	7	US-11-096-568A-14679	Sequence 14679, A	780	31	34.8	1098	7	US-11-072-512-2475	Sequence 2475, Ap
708	31	34.8	471	7	US-11-024-959-419	Sequence 419, App	781	31	34.8	1116	7	US-11-113-751-32	Sequence 32, Appl
709	31	34.8	473	7	US-11-087-099-1665	Sequence 1665, App	782	31	34.8	1116	7	US-11-113-751-34	Sequence 34, Appl
710	31	34.8	473	7	US-11-087-099-1819	Sequence 1819, App	783	31	34.8	1118	7	US-11-113-751-42	Sequence 42, Appl
711	31	34.8	474	7	US-11-096-568A-27009	Sequence 27009, A	784	31	34.8	1121	7	US-11-113-751-19	Sequence 19, Appl
712	31	34.8	476	7	US-11-024-959-292	Sequence 292, App	785	31	34.8	1151	7	US-11-113-751-36	Sequence 36, Appl
713	31	34.8	476	7	US-11-096-568A-10398	Sequence 10398, A	786	31	34.8	1153	7	US-11-113-751-44	Sequence 44, Appl
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; Publication No. US20060048240A1
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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
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; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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US-11-207-078-302
; Sequence 302, Application US/11207078
; Publication No. US20060040307A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCE: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/207,078
; FILING DATE: 17-Aug-2005
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,477
; FILING DATE: 22-Nov-2000
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
```

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 302:
US-11-207-078-302

Query Match 48.3%; Score 43; DB 7; Length 54;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 WEVLCWTW 8
DB 18 WAPLCWAW 25

RESULT 4
US-11-055-822-130
Sequence 130, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPCN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 130
LENGTH: 361
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-130

Query Match 48.3%; Score 43; DB 7; Length 361;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 EVLCLWTW 8
DB 76 EVLCLWIW 82

RESULT 5
US-10-934-944-216
Sequence 216, Application US/10934944
Publication No. US20060037096A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongmei
TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
FILE REFERENCE: 07678/141008
CURRENT APPLICATION NUMBER: US/10/934,944
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 10/686,947
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 10/387,346
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: 10/340,861
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 10/293,252
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/418,933
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/363,684
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/347,444
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/337,684
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.3
SEQ ID NO 216
LENGTH: 521
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-10-934-944-216

Query Match 48.3%; Score 43; DB 6; Length 521;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
DB 23 WELLKWIWIKPKLESCLR 41

RESULT 6
US-10-934-944-264
Sequence 264, Application US/10934944
Publication No. US20060037096A1
GENERAL INFORMATION:
APPLICANT: Xu, Dongmei
TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
FILE REFERENCE: 07678/141008
CURRENT APPLICATION NUMBER: US/10/934,944
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 10/686,947
PRIOR FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/503,989
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/485,368
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 10/387,346
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: 10/340,861
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 10/293,252

;; PRIOR FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: 60/418,933
;; PRIOR FILING DATE: 2002-10-16
;; PRIOR APPLICATION NUMBER: 60/363,684
;; PRIOR FILING DATE: 2002-03-12
;; PRIOR APPLICATION NUMBER: 60/347,444
;; PRIOR FILING DATE: 2002-01-11
;; PRIOR APPLICATION NUMBER: 60/337,684
;; PRIOR FILING DATE: 2001-11-13
;; NUMBER OF SEQ ID NOS: 387
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 264
;; LENGTH: 521
;; TYPE: PRT
;; ORGANISM: Nicotiana tabacum
US-10-934-944-264

Query Match 48.3%; Score 43; DB 6; Length 521;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
||:|:|:|:|:|:|:|:|:|:
Db 23 WELLKWIWIKPKKLESCLR 41

RESULT 7
US-11-116-881A-225
; Sequence 225, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-273

Query Match 48.3%; Score 43; DB 7; Length 521;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
||:|:|:|:|:|:|:|:|:|:
Db 23 WELLKWIWIKPKKLESCLR 41

RESULT 9
US-11-089-551A-32
; Sequence 32, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT APPLICATION NUMBER: US/11/089,551A
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/559,286
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-32

Query Match 47.8%; Score 42.5; DB 7; Length 750;
Best Local Similarity 66.7%; Pred. No. 74;


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Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 5 CW-TWETCE 12
DB 510 CWGTWDTC 518

RESULT 10
US-11-096-568A-30667
; Sequence 30667, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30667
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(405)
; OTHER INFORMATION: Ceres Seq. ID no. 4968873
US-11-096-568A-30667

Query Match 47.2%; Score 42; DB 7; Length 405;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WEVLCWTWE 9
DB 245 WESTCWTYD 253

RESULT 11
US-11-096-568A-30666
; Sequence 30666, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30666
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(438)
; OTHER INFORMATION: Ceres Seq. ID no. 4968872
US-11-096-568A-30666

Query Match 47.2%; Score 42; DB 7; Length 438;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WEVLCWTWE 9
DB 278 WESTCWTYD 286

RESULT 12
US-11-096-568A-30665
; Sequence 30665, Application US/11096568A
; Publication No. US20060048240A1
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; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 30665
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(447)
; OTHER INFORMATION: Ceres Seq. ID no. 4968871
US-11-096-568A-30665

Query Match 47.2%; Score 42; DB 7; Length 447;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 WEVLCWTWE 9
DB 287 WESTCWTYD 295

RESULT 13
US-10-975-798-4
; Sequence 4, Application US/10975798
; Publication No. US20050250090A1
; GENERAL INFORMATION:
; APPLICANT: Edward Kaftan
; APPLICANT: Adrienne Dubin
; APPLICANT: Sandy Chaplan
; TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT
; FILE REFERENCE: PRD2142
; CURRENT APPLICATION NUMBER: US/10/975,798
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-798-4

Query Match 47.2%; Score 42; DB 6; Length 579;
Best Local Similarity 46.2%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 WEVLCWTWETCER 13
DB 322 WIAAWTVRACER 334

RESULT 14
US-10-975-798-3
; Sequence 3, Application US/10975798
; Publication No. US20050250090A1
; GENERAL INFORMATION:
; APPLICANT: Edward Kaftan
; APPLICANT: Adrienne Dubin
; APPLICANT: Sandy Chaplan
; TITLE OF INVENTION: ASSAY SYSTEMS AND METHODS FOR DETECTING MOLECULES THAT INTERACT
; FILE REFERENCE: PRD2142
; CURRENT APPLICATION NUMBER: US/10/975,798
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
```

; LENGTH: 580
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-798-3

Query Match 47.2%; Score 42; DB 6; Length 580;
Best Local Similarity 46.2%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
| : |||||
Db 323 WIIAAWTVRACER 335

RESULT 15

US-10-613-744-10
; Sequence 10, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-10

Query Match 47.2%; Score 42; DB 6; Length 731;
Best Local Similarity 46.2%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
| : |||||
Db 471 WIIAAWTVRACER 483

RESULT 16

US-11-009-658-6
; Sequence 6, Application US/11009658
; Publication No. US2006000340A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BB1332
; CURRENT APPLICATION NUMBER: US/11/009,658
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US/09/914,098
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-009-658-6

Query Match 46.1%; Score 41; DB 7; Length 231;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 WEVLC--WTWE 9
| : |||||
Db 157 MAVVCDVMSWE 167

RESULT 17

US-11-096-568A-17867
; Sequence 17867, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17867
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(296)
; OTHER INFORMATION: Ceres Seq. ID no. 12361390
US-11-096-568A-17867

Query Match 46.1%; Score 41; DB 7; Length 296;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CWTWET 10
| |||||
Db 197 CWTWET 202

RESULT 18

US-10-934-944-284
; Sequence 284, Application US/10934944
; Publication No. US20060037096A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
; FILE REFERENCE: 07678/141008
; CURRENT APPLICATION NUMBER: US/10/934,944
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/686,947
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 10/387,346
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 10/340,861
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.3

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/ SEQ ID NO 284
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Nicotiana tabacum
US-10-934-944-284

Query Match          46.1%; Score 41; DB 6; Length 458;
Best Local Similarity 42.1%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
   ||| ||| ||| |||
Db 21 WKVLNNAWFGPKMEKCLR 39

RESULT 19
US-11-116-881A-293
/ Sequence 293, Application US/11116881A
/ Publication No. US20060041949A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Dongmei
/ TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
/ FILE REFERENCE: 07678/141014
/ CURRENT APPLICATION NUMBER: US/11/116,881A
/ CURRENT FILING DATE: 2005-04-27
/ PRIOR APPLICATION NUMBER: 60/665,451
/ PRIOR FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/665,097
/ PRIOR FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/646,764
/ PRIOR FILING DATE: 2005-01-25
/ PRIOR APPLICATION NUMBER: 60/607,357
/ PRIOR FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 60/566,235
/ PRIOR FILING DATE: 2004-04-29
/ PRIOR APPLICATION NUMBER: 10/934,944
/ PRIOR FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 10/943,507
/ PRIOR FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 10/943,507
/ PRIOR FILING DATE: 2004-09-17
/ PRIOR APPLICATION NUMBER: 60/503,989
/ PRIOR FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/485,368
/ PRIOR FILING DATE: 2003-07-08
/ PRIOR APPLICATION NUMBER: 60/418,933
/ PRIOR FILING DATE: 2002-10-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2300
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 293
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Nicotiana tabacum
US-11-116-881A-293

Query Match          46.1%; Score 41; DB 7; Length 458;
Best Local Similarity 42.1%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
   ||| ||| ||| |||
Db 21 WKVLNNAWFGPKMEKCLR 39

RESULT 20
US-10-934-944-278
/ Sequence 278, Application US/10934944
/ Publication No. US20060037096A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Dongmei
/ TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
/ FILE REFERENCE: 07678/141008
/ CURRENT APPLICATION NUMBER: US/10/934,944
```

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/ CURRENT FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 10/686,947
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: 60/503,989
/ PRIOR FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/485,368
/ PRIOR FILING DATE: 2003-07-08
/ PRIOR APPLICATION NUMBER: 10/387,346
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: 10/340,861
/ PRIOR FILING DATE: 2003-01-10
/ PRIOR APPLICATION NUMBER: 10/293,252
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: 60/418,933
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: 60/363,684
/ PRIOR FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/347,444
/ PRIOR FILING DATE: 2002-01-11
/ PRIOR APPLICATION NUMBER: 60/337,684
/ PRIOR FILING DATE: 2001-11-13
/ NUMBER OF SEQ ID NOS: 387
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 278
/ LENGTH: 516
/ TYPE: PRT
/ ORGANISM: Nicotiana tabacum
US-10-934-944-278

Query Match          46.1%; Score 41; DB 6; Length 516;
Best Local Similarity 42.1%; Pred. No. 90;
Matches 8; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY 1 WEVLCWTW-----ETCER 13
   ||| ||| ||| |||
Db 21 WKVLNNAWFGPKMEKCLR 39

RESULT 21
US-11-116-881A-287
/ Sequence 287, Application US/11116881A
/ Publication No. US20060041949A1
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Dongmei
/ TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
/ FILE REFERENCE: 07678/141014
/ CURRENT APPLICATION NUMBER: US/11/116,881A
/ CURRENT FILING DATE: 2005-04-27
/ PRIOR APPLICATION NUMBER: 60/665,451
/ PRIOR FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/665,097
/ PRIOR FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/646,764
/ PRIOR FILING DATE: 2005-01-25
/ PRIOR APPLICATION NUMBER: 60/607,357
/ PRIOR FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 60/566,235
/ PRIOR FILING DATE: 2004-04-29
/ PRIOR APPLICATION NUMBER: 10/934,944
/ PRIOR FILING DATE: 2004-09-03
/ PRIOR APPLICATION NUMBER: 10/943,507
/ PRIOR FILING DATE: 2004-09-17
/ PRIOR APPLICATION NUMBER: 60/503,989
/ PRIOR FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/485,368
/ PRIOR FILING DATE: 2003-07-08
/ PRIOR APPLICATION NUMBER: 60/418,933
/ PRIOR FILING DATE: 2002-10-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2300
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 287
```

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; LENGTH: 516
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-287

Query Match      46.1%; Score 41; DB 7; Length 516;
Best Local Similarity 42.1%; Pred.No. 90;
Matches      8; Conservative 1; Mismatches 4; Indels 6; Gaps 1;

QY      1 WEVLCWTW-----ETCER 13
      ||| ||| ||| ||| |||
Db      21 WKVLNWAWFGPKWKEKCLR 39

RESULT 22
US-11-000-463-750
; Sequence 750, Application US/110000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 750
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-750

Query Match      45.5%; Score 40.5; DB 7; Length 106;
Best Local Similarity 50.0%; Pred.No. 35;
Matches      7; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY      1 WEVLCW-----TWE 9
      ||| ||| |||
Db      16 WELLAWIQLNLTWE 29

RESULT 23
US-11-000-463-751
; Sequence 751, Application US/110000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod

```

```
RESULT 25
US-11-098-686-10766
; Sequence 10766, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10766
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10766
Query Match 44.9%; Score 40; DB 7; Length 271;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLQWTWE 9
||| ||| :|
Db 95 WETLCGSWK 103

RESULT 26
US-11-096-568A-24136
; Sequence 24136, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24136
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(291)
; OTHER INFORMATION: Ceres Seq. ID no. 12419132
US-11-096-568A-24136
Query Match 44.9%; Score 40; DB 7; Length 291;
Best Local Similarity 50.0%; Pred. No. 83;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 WEVL--CWTWETCE 12
||| ||| :|
Db 216 WRVLGFLSWSCE 229

RESULT 27
US-11-096-568A-24135
; Sequence 24135, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
```

```
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 24135
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(460)
; OTHER INFORMATION: Ceres Seq. ID no. 12419131
US-11-096-568A-24135
Query Match 44.9%; Score 40; DB 7; Length 460;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 WEVL--CWTWETCE 12
||| ||| :|
Db 385 WRVLGFLSWSCE 398

RESULT 28
US-11-087-099-8792
; Sequence 8792, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8792
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-11-087-099-8792
Query Match 44.9%; Score 40; DB 7; Length 491;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LCWTWE 9
: ||| :
Db 222 ICWTWQ 227

RESULT 29
US-10-501-035-215
; Sequence 215, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-215
Query Match 44.9%; Score 40; DB 6; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(273)
; OTHER INFORMATION: Ceres Seq. ID no. 13604319
US-11-096-568A-33844

Query Match      43.8%; Score 39; DB 7; Length 273;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 EVLCWTWETCE 12
Db      45 DALNWIWKACE 55

RESULT 34
US-11-096-568A-33843
; Sequence 33843, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33843
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(287)
; OTHER INFORMATION: Ceres Seq. ID no. 13604318
US-11-096-568A-33843

Query Match      43.8%; Score 39; DB 7; Length 287;
Best Local Similarity 45.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 EVLCWTWETCE 12
Db      59 DALNWIWKACE 69

RESULT 35
US-11-096-568A-17128
; Sequence 17128, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 17128
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(302)
; OTHER INFORMATION: Ceres Seq. ID no. 12356114
US-11-096-568A-17128

Query Match      43.8%; Score 39; DB 7; Length 302;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

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QY      2 EVLCWTWETCE 12
Db      119 EVLCWSEDSAE 129

RESULT 36
US-11-096-568A-33842
; Sequence 33842, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33842
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(308)
; OTHER INFORMATION: Ceres Seq. ID no. 13604317
US-11-096-568A-33842

Query Match      43.8%; Score 39; DB 7; Length 308;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 EVLCWTWETCE 12
Db      80 DALNWIWKACE 90

RESULT 37
US-10-980-388-117
; Sequence 117, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
```

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 117
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-117

Query Match 43.8%; Score 39; DB 6; Length 340;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLCTWTE 9
:|:|:
Db 220 ILCYTWE 226

RESULT 38

US-11-127-877-53

; Sequence 53, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT FILING DATE: 2005-03-12
; PRIOR APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2004-05-12
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (245)..(245)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-127-877-53

Query Match 43.8%; Score 39; DB 7; Length 340;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLCTWTE 9
:|:|:
Db 220 ILCYTWE 226

RESULT 39

US-11-096-568A-31101

; Sequence 31101, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31101
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 4989670
US-11-096-568A-31101

Query Match 43.8%; Score 39; DB 7; Length 353;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 12
||:|:
Db 254 WEILMEGWKCE 265

RESULT 40

US-11-096-568A-31100

; Sequence 31100, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31100
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: Ceres Seq. ID no. 4989669
US-11-096-568A-31100

Query Match 43.8%; Score 39; DB 7; Length 396;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 12
||:|:
Db 297 WEILMEGWKCE 308

RESULT 41

US-11-096-568A-27975

; Sequence 27975, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27975
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc_feature
; LOCATION: (1)..(399)
; OTHER INFORMATION: Ceres Seq. ID no. 2156313
US-11-096-568A-27975

Query Match 43.8%; Score 39; DB 7; Length 399;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCE 12


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Db          ||:| | ||
           300 WEILMEGWKCE 311

RESULT 42
US-11-096-568A-31099
; Sequence 31099, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 31099
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(399)
; OTHER INFORMATION: Ceres Seq. ID no. 4989668
US-11-096-568A-31099

Query Match      43.8%; Score 39; DB 7; Length 399;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCE 12
        ||:| | ||
Db      300 WEILMEGWKCE 311

RESULT 43
US-11-096-568A-27974
; Sequence 27974, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27974
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(400)
; OTHER INFORMATION: Ceres Seq. ID no. 2156312
US-11-096-568A-27974

Query Match      43.8%; Score 39; DB 7; Length 400;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCE 12
        ||:| | ||
Db      301 WEILMEGWKCE 312

RESULT 44
US-11-096-568A-27973
; Sequence 27973, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

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; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27973
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(491)
; OTHER INFORMATION: Ceres Seq. ID no. 2156311
US-11-096-568A-27973

Query Match      43.8%; Score 39; DB 7; Length 491;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 WEVLCWTWETCE 12
        ||:| | ||
Db      392 WEILMEGWKCE 403

RESULT 45
US-11-087-099-8500
; Sequence 8500, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8500
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-8500

Query Match      43.8%; Score 39; DB 7; Length 542;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 LCWTWE 9
        ||| ||
Db      274 LCWLWE 279

RESULT 46
US-11-096-568A-14533
; Sequence 14533, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14533
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(106)
; OTHER INFORMATION: Ceres Seq. ID no. 6410188
US-11-096-568A-14533

Query Match      42.7%; Score 38; DB 7; Length 106;
```

```
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLQWTWTC 11
Db 32 WGLRCSAWPTC 42

RESULT 47
US-11-096-568A-15779
; Sequence 15779, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 15779
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 12348322
US-11-096-568A-15779

Query Match 42.7%; Score 38; DB 7; Length 107;
Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLQWTWTC 11
Db 33 WGLRCSAWPTC 43

RESULT 48
US-11-072-512-2829
; Sequence 2829, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2829

Best Local Similarity 45.5%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 WEVLQWTWTC 11
Db 33 WGLRCSAWPTC 43

RESULT 49
US-10-934-944-286
; Sequence 286, Application US/10934944
; Publication No. US20060037096A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Cloning of Cytochrome P450 Genes From Nicotiana
; FILE REFERENCE: 07678/141008
; CURRENT APPLICATION NUMBER: US/10/934,944
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/686,947
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 10/387,346
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 10/340,861
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 286
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-934-944-286

Query Match 42.7%; Score 38; DB 6; Length 304;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WEVLQWTW 8
Db 24 WRVLNWNV 31

RESULT 50
US-11-116-881A-295
; Sequence 295, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
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Wed Mar 29 08:58:02 2006

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; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 295
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-116-881A-295

Query Match      42.7%; Score 38; DB 7; Length 304;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 WEVLQWTW 8
Db      24 WRVLNWWV 31

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Search completed: March 28, 2006, 11:55:45
Job time : 29 secs

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